

This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

As rescanning documents *will not* correct images,
please do not report the images to the
Image Problem Mailbox.

THIS PAGE BLANK (USPTO)

STIC-Biotech/Ch mLib

59945

From: Hutzell, Paula
Sent: Friday, February 08, 2002 12:22 PM
To: STIC-Biotech/ChemLib; Graser, Jennifer
Subject: FW: rush search
Importance: High

approved

-----Original Message-----

Fr m: Graser, Jennifer
Sent: Friday, February 08, 2002 12:20 PM
T : Hutzell, Paula
Subject: rush search
Imp rtance: High

Hi Paula,
Could you please authorize the following rush search?
Thanks,
Jennifer

STIC:
Please search SEQ ID NOs: 4, 6, 8, and 10 from 09/865,159 in pending and commercial databases.
Thanks,
Jennifer Graser
CM1 7E09 (mailbox 7E12)
1645
308-1742

CRFE

Point of Contact:
Toby Port
Technical Info. Specialist
CM1 1E01 TEL: 308-3534

6A04

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 2/8
Date Completed: 2/8
Searcher Prep/Review: 10
Clerical: _____
Online time: 10

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: 4
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST(where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: gf
WWW/Internet: _____
Other (specify): _____

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 8, 2002, 15:23:15 ; Search time 67.74 Seconds

(without alignments)
134.500 Million cell updates/sec

Title: US-09-865-159-4

Perfect score: 631

Sequence: 1 ALEGTFAFASGASALASVN.....GLMKCTSDQDEQFIPKCSR 123

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database :

Listing first 45 summaries

```

1: /SIDS8/gcgdata/geneseq/geneseq/AA1980.DAT:*
2: /SIDS8/gcgdata/geneseq/geneseq/AA1981.DAT:*
3: /SIDS8/gcgdata/geneseq/geneseq/AA1982.DAT:*
4: /SIDS8/gcgdata/geneseq/geneseq/AA1983.DAT:*
5: /SIDS8/gcgdata/geneseq/geneseq/AA1984.DAT:*
6: /SIDS8/gcgdata/geneseq/geneseq/AA1985.DAT:*
7: /SIDS8/gcgdata/geneseq/geneseq/AA1986.DAT:*
8: /SIDS8/gcgdata/geneseq/geneseq/AA1987.DAT:*
9: /SIDS8/gcgdata/geneseq/geneseq/AA1988.DAT:*
10: /SIDS8/gcgdata/geneseq/geneseq/AA1989.DAT:*
11: /SIDS8/gcgdata/geneseq/geneseq/AA1990.DAT:*
12: /SIDS8/gcgdata/geneseq/geneseq/AA1991.DAT:*
13: /SIDS8/gcgdata/geneseq/geneseq/AA1992.DAT:*
14: /SIDS8/gcgdata/geneseq/geneseq/AA1993.DAT:*
15: /SIDS8/gcgdata/geneseq/geneseq/AA1994.DAT:*
16: /SIDS8/gcgdata/geneseq/geneseq/AA1995.DAT:*
17: /SIDS8/gcgdata/geneseq/geneseq/AA1996.DAT:*
18: /SIDS8/gcgdata/geneseq/geneseq/AA1997.DAT:*
19: /SIDS8/gcgdata/geneseq/geneseq/AA1998.DAT:*
20: /SIDS8/gcgdata/geneseq/geneseq/AA1999.DAT:*
21: /SIDS8/gcgdata/geneseq/geneseq/AA2000.DAT:*
22: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	631	100.0	123	AAV44376	Exemplary truncate
2	612.5	97.1	169	AAV44381	P. aeruginosa E coli
3	611	96.8	169	AAV44380	P. aeruginosa H co
4	325.5	51.6	122	AAV44377	Exemplary truncate
5	307	48.7	168	AAV44385	P. aeruginosa F coli
6	305.5	48.4	168	AAV44384	P. aeruginosa H co
7	147	23.3	127	AAV44379	Exemplary truncate
8	146	23.1	129	AAV44375	Exemplary truncate
9	134	21.2	127	AAV44378	Exemplary truncate
10	127.5	20.2	175	AAV44383	P. aeruginosa E coli
11	126	20.0	175	AAV44382	P. aeruginosa H co

ALIGNMENTS

RESULT 1	AAV44376	AAV44376 standard; Protein: 123 AA.	12	106.5	16.9	53	14	AA838503	P. aeruginosa pill
ID	AAV44376		13	96	15.2	17	13	AA825828	P. aeruginosa PAK mu
AC	AAV44376;		14	93	14.7	17	13	AA825908	P. aeruginosa PAK pl
DT	14-MAR-2000 (first entry)		15	93	14.7	17	17	AA897575	MAB PK99H antigen,
XX			16	93	14.7	17	17	AA888398	B-cell antigen PAK
DE	Exemplary truncated P. aeruginosa PAK pillin protein.		17	93	14.7	17	17	AA886703	Pillin derived pep
XX			18	93	14.7	17	17	AA894018	PAK pillin epitope
OS	Pseudomonas aeruginosa.		19	93	14.7	17	18	AA837491	Pseudomonas aerigl
XX			20	93	14.7	17	17	AA826965	PAK pillin peptide.
XX			21	93	14.7	17	21	AAV49350	P. aeruginosa PAK
XX			22	93	14.7	17	21	AAV49356	Cell surface bindi
XX			23	88	13.9	17	21	AAV49356	P. aeruginosa PAK
XX			24	87	13.8	17	21	AAV49357	P. aeruginosa PAK
XX			25	87	13.8	17	21	AAV49357	P. aeruginosa PAK
XX			26	84	13.3	3588	14	AA834712	Bacillus subtilis
XX			27	82	13.0	14	11	AA808100	PAK polypeptide de
XX			28	82	13.0	14	17	AA86709	Residues 131-143 o
XX			29	81	12.8	17	21	AAV49352	P. aeruginosa PAK
XX			30	80	12.7	17	21	AAV49353	P. aeruginosa PAK
XX			31	75	11.9	17	21	AAV49354	P. aeruginosa PAK
XX			32	75	11.9	1073	21	AA801837	Haemophilus influe
XX			33	75	11.9	1079	21	AA801836	Haemophilus influe
XX			34	74	11.7	585	22	AA832278	C glutamincum prote
XX			35	74	11.7	692	22	AAU04851	Microspora eve
XX			36	73.5	11.6	199	21	AA806414	Arabidopsis thalia
XX			37	73.5	11.6	199	21	AA851601	Arabidopsis thalia
XX			38	73.5	11.6	231	21	AAV90920	Cenarchaeum symbio
XX			39	73.5	11.6	238	21	AA806413	Arabidopsis thalia
XX			40	73.5	11.6	238	21	AA851600	Arabidopsis thalia
XX			41	73.5	11.6	243	21	AA806412	Arabidopsis thalia
XX			42	73.5	11.6	243	21	AA851599	Arabidopsis thalia
XX			43	73.5	11.6	945	22	AA879309	Corynebacterium gl
XX			44	73.5	11.6	948	22	AA832286	C glutamincum prote
XX			45	73.5	11.6	948	22	AA879308	Corynebacterium gl

Claim 9; Fig 1B; 32pp; English.

XX The present sequence is the modified PAK pilin protein from
CC P. aeruginosa. The N-terminal peptide region preferably lacks the first
CC 15-40 residues of native P. aeruginosa. Modified pilin proteins are
CC prepared by PCR amplification of pilin coding sequences using primers
CC that effect the desired deletion, modification or insertion of a coiled-
CC coil moiety in the coding sequences. The modified protein thus lacks a
CC critical alpha-helical forming portion. This prevents oligomerisation of
CC pilin protein necessary for attachment to the host cell during infection.
CC The ligated plasmid DNA was transformed into an expression host. The
CC modified pilin protein is useful in treatment and prophylaxis for
CC individuals at risk of Pseudomonas infection, e.g. cystic fibrosis
CC patients, burn patients, and severe neutropenic patients.
CC
SQ Sequence 123 AA:

Query Match 100.0%; Score 631; DB 21; Length 123;
Best Local Similarity 100.0%; Pred. No. 1.3e-62;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALEGTFFARSEGASALASVNPILKTVEEALSRGMSYKSGTGEDATKKEVPLGVADANK 60
Db 1 alegtffarsegasalaasvnpilktveealstrgmsykgltgedatkkevplgvadank 60
OY 61 LGTIALKPPADGTADITLFTFMGAGAPRNKGIITLFTADGLMKTSDDEQFI 120
Db 61 lgtialkppadgtaditlftfmgagaprnkgiitlftadglwktcsdqdeqfi 120
OY 121 CSR 123
Db 121 csr 123

RESULT 2
AAV44381
ID AAV44381 standard; Protein; 169 AA.

XX AAV44381;

DT 14-MAR-2000 (first entry)

DE P. aeruginosa E coil-truncated PAK pilin protein.

XX Modified PAK pilin protein; alpha-helical forming portion; E coil;
KW Exemplary coil; coiled coil heterodimer; host cell-receptor site;
KW Pseudomonas infection; cystic fibrosis; neutropenia.

OS Pseudomonas aeruginosa.

XX W09965511-A2.

PD 23-DEC-1999.

PF 11-JUN-1999; 99WO-CA00554.

PR 12-JUN-1998; 98US-0089155.

XX (UYAL-) UNIV ALBERTA.

PI Hodges RS, Irvlin RV;

DR WPI; 2000-106013/09.

DR N-PSDB; AA229540.

PT Composition for treating or preventing Pseudomonas aeruginosa infection
XX comprising pilin protein that can not self-assemble -

XX Claim 1; Fig 3B; 32pp; English.

XX The present sequence encodes E coil truncated PAK pilin protein from
CC P. aeruginosa. The first 15-40 residues of the N-terminal peptide region
CC is replaced by a peptide segment capable of forming a coiled-coil

CC heterodimer with an oppositely charged peptide segment which can form
CC dimeric structures. These proteins are less inflammatory due to reduced
CC degree of mobilisation of host-cell receptor sites. This prevents
CC oligomerisation of pilin protein necessary for attachment to the host
CC cell during infection. The modified pilin protein is useful in treatment
CC and prophylaxis for individuals at risk of Pseudomonas infection,
CC e.g. cystic fibrosis patients, burn patients, and severe neutropenic
CC patients.
CC
SQ Sequence 169 AA:

Query Match 97.1%; Score 612.5; DB 21; Length 169;
Best Local Similarity 96.8%; Pred. No. 2.2e-60;
Matches 122; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

OY 1 ALEGTFFARSEGASALASVNPILKTVEEALSRGMSYKSGTGEDATKKEVPLGVAD 57
Db 44 alekggggfarsegasalaasvnpilktveealstrgmsykgltgedatkkevplgvad 103
OY 58 ANKLGITIALKPPADGTADITLFTFMGAGAPRNKGIITLFTADGLMKTSDDEQFI 117
Db 104 ankligtialkppadgtaditlftfmgagaprnkgiitlftadglwktcsdqdeqfi 163
OY 118 PKGCSR 123
Db 164 pkgcsr 169

RESULT 3
AAV44380
ID AAV44380 standard; Protein; 169 AA.

XX AAV44380;

DT 14-MAR-2000 (first entry)

DE P. aeruginosa H coil-truncated PAK pilin protein.

XX Modified PAK pilin protein; alpha-helical forming portion;
KW coiled coil homodimer; host cell-receptor site; Pseudomonas infection;
KW cystic fibrosis; neutropenia.

OS Pseudomonas aeruginosa.

XX W09965511-A2.

PD 23-DEC-1999.

PF 11-JUN-1999; 99WO-CA00554.

PR 12-JUN-1998; 98US-0089155.

XX (UYAL-) UNIV ALBERTA.

PI Hodges RS, Irvlin RT;

DR WPI; 2000-106013/09.

DR N-PSDB; AA229539.

PT Composition for treating or preventing Pseudomonas aeruginosa infection
XX comprising pilin protein that can not self-assemble -
XX Claim 1; Fig 3A; 32pp; English.

XX The present sequence is the H coil truncated PAK pilin protein from
CC P. aeruginosa. The first 15-40 residues of the N-terminal peptide region
CC is replaced by a peptide segment capable of forming a coiled-coil
CC homodimer with an identical peptide segment which can form dimeric
CC structures. These proteins are less inflammatory due to reduced degree of
CC mobilisation of host-cell receptor sites. This prevents oligomerisation
CC of pilin protein necessary for attachment to the host cell during
CC infection. The modified pilin protein is useful in treatment and

CC prophylaxis for individuals at risk of Pseudomonas infection,
 CC e.g. cystic fibrosis patients, burn patients, and severe neutropenic
 CC patients.
 XX
 SO Sequence 169 AA;

Query Match 96.8%; Score 611; DB 21; Length 169;
 Best Local Similarity 99.2%; Pred. No. 3.3e-60;
 Matches 119; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 GTEFARSGASALASVNPDKTVEALSRGWSVSGCTEDATKREVLGYAADANKIGT 63
 |||
 Db 50 ggefarsegasalasvnpdkltveealstrgwsvsgtgedatckevplgyaadanlkigt 109
 OY 64 IALKPDPADGTADITLTFTMGAGCPKNNKGIITLTTRTADGLMKCTSDODEQFIKGCSSR 123
 |||
 Db 110 ialkpdpadgtditltftmgagcpkngkiltlttrtaadglmwkctsdqdeqfilpkgcscr 169

RESULT 4
 ID AAY44377 standard; Protein: 122 AA.
 XX

AC AAY44377;
 XX
 DT 14-MAR-2000 (first entry)
 XX

DE Exemplary truncated P. aeruginosa PAO pilin protein.

XX Modified PAO pilin protein; alpha-helical forming portion;
 KW Pseudomonas infection; cystic fibrosis; neutropenia.

XX Pseudomonas aeruginosa.

XX WO965511-A2.

XX PD 23-DEC-1999.

XX PF 11-JUN-1999; 99WO-CA00554.

XX PR 12-JUN-1998; 98US-0089155.

XX PA (UYAL-) UNIV ALBERTA.

XX PI Hodges RS, Irvin RT;

XX DR WPI: 2000-106013/09.

XX DR N-PSDB; AA229536.

XX PT Composition for treating or preventing Pseudomonas aeruginosa infection
 comprising pilin protein that can not self-assemble -

XX PS Claim 9; Fig 1C; 32pp; English.

XX The present sequence is the modified PAO pilin protein from
 CC P.aeruginosa. The N-terminal peptide region preferably lacks the first
 CC 15-40 residues of native P.aeruginosa. Modified pilin proteins are
 CC prepared by PCR amplification of pilin coding sequences using primers
 CC that effect the desired deletion, modification or insertion of a coiled-
 CC coil moiety in the coding sequences. The modified protein thus lacks a
 CC critical alpha-helical forming portion. This prevents oligomerisation of
 CC pilin protein necessary for attachment to the host cell during infection.
 CC The ligated plasmid DNA was transformed into an expression host. The
 CC modified pilin protein is useful in treatment and prophylaxis for
 CC individuals at risk of Pseudomonas infection, e.g. cystic fibrosis
 CC patients, burn patients, and severe neutropenic patients.

XX Sequence 122 AA;

Query Match 51.6%; Score 325.5; DB 21; Length 122;
 Best Local Similarity 60.2%; Pred. No. 1.3e-28;

Matches 74; Conservative 11; Mismatches 31; Indels 7; Gaps 4;

OY 1 ALEGTFAFSGASALASVNPDKTVEALSRGWSVSGCTEDATKREVLGYAAD 57
 |||
 Db 1 alegtefarsegasalasvnpdkltveealstrgwsvsgtgedatckevplgyaadanlkigt 58
 OY 58 ANKIUGTIALKFPDPADGTADITLTFTMGAGCPKNNKGIITLTTRTADGLMKCTSDODEQFI 117
 |||
 Db 59 ankiugvlaaveds-gagdlftltqgtcspsknaikviltlnt-adywackstqdpnft 116

OY 118 PKG 120
 |||
 Db 117 pkg 119

RESULT 5
 ID AAY44385 standard; Protein: 168 AA.
 XX

AC AAY44385;
 XX

DT 14-MAR-2000 (first entry)
 XX

DE P.aeruginosa E coil-truncated PAO pilin protein.

XX Modified PAO pilin protein; alpha-helical forming portion; E coil;
 KW Exemplary coil; coiled coil heterodimer; host cell-receptor site;
 KW Pseudomonas infection; cystic fibrosis; neutropenia.

XX Pseudomonas aeruginosa.

XX WO965511-A2.

XX PD 23-DEC-1999.

XX PF 11-JUN-1999; 99WO-CA00554.

XX PR 12-JUN-1998; 98US-0089155.

XX PA (UYAL-) UNIV ALBERTA.

XX PI Hodges RS, Irvin RT;

XX DR WPI: 2000-106013/09.

XX DR N-PSDB; AA229544.

XX PT Composition for treating or preventing Pseudomonas aeruginosa infection
 comprising pilin protein that can not self-assemble -

XX PS Claim 1; Fig 5B; 32pp; English.

XX The present sequence encodes E coil truncated PAO pilin protein from
 CC P.aeruginosa. The first 15-40 residues of the N-terminal peptide region
 CC is replaced by a peptide segment capable of forming a coiled-coil
 CC heterodimer with an oppositely charged peptide segment which can form
 CC dimeric structures. These proteins are less inflammatory due to reduced
 CC degree of mobilisation of host-cell receptor sites. This prevents
 CC oligomerisation of pilin protein necessary for attachment to the host
 CC cell during infection. The modified pilin protein is useful in treatment
 CC and prophylaxis for individuals at risk of Pseudomonas infection,
 CC e.g. cystic fibrosis patients, burn patients, and severe neutropenic
 CC patients.

XX Sequence 168 AA;

Query Match 48.7%; Score 307; DB 21; Length 168;
 Best Local Similarity 57.9%; Pred. No. 2.3e-26;
 Matches 73; Conservative 11; Mismatches 33; Indels 10; Gaps 5;

OY 1 ALE---GTEFARSGASALASVNPDKTVEALSRGWSVSGCTEDATKREVLGY 54
 |||
 Db 44 alekggsefarsegasalasvnpdkltveealstrgwsvsgtgedatckevplgy 101

RAY443/5

XX

[illegible][illegible]

XX 11-JUN-1999; 99WO-CA00554.
 XX
 PR 12-JUN-1998; 98US-0089155.
 XX
 PA (UYAL-) UNIV ALBERTA.
 XX
 PI Hodges RS, Irvin RT;
 XX
 DR WPI: 2000-106013/09.
 DR N-PSDB; AA229542.
 XX
 PT Composition for treating or preventing *Pseudomonas aeruginosa* infection
 PT comprising pilin protein that can not self-assemble -
 XX
 PS Claim 1; Fig 4B; 32pp; English.

CC The present sequence encodes E coil truncated K122 pilin protein from
 CC *P. aeruginosa*. The first 15-40 residues of the N-terminal peptide region
 CC is replaced by a peptide segment capable of forming a coiled-coil
 CC heterodimer with an oppositely charged peptide segment which can form
 CC dimeric structures. These proteins are less inflammatory due to reduced
 CC degree of mobilisation of pilin protein necessary for attachment to the host
 CC cell during infection. The modified pilin protein is useful in treatment
 CC and prophylaxis for individuals at risk of *Pseudomonas* infection.
 CC e.g. cystic fibrosis patients, burn patients, and severe neutropenic
 CC patients.

SO Sequence 175 AA;

Query Match 20.2%; Score 127.5; DB 21; Length 175;
 Best Local Similarity 30.2%; Pred. No. 2.4e-06;
 Matches 39; Conservative 17; Mismatches 60; Indels 13; Gaps 4;

QY 1 ALE---CTEFARSEGASALASVNP...LKTVEALSRGWSVKS...GTGTEADATKKEVPLG--VA 55
 Db 44 alekgggggetaraqlsermtlasgltkvsdlfsgdscpantaatagiektdtinkkyv 103
 QY 56 ADANKLGTALKPDPADGTADITLFTMGAGPKNKGIITLTFTAADG---LTKCTSDQ 112
 Db 104 akvtgtgtaa-----assgctvalmkasdvatpigrkltlilgnadkgsylwactstna 158
 QY 113 DEQFTPKGC 121
 Db 159 dnkylpktc 167

RESULT 11

AAV44382
 ID AAV44382 standard; Protein; 175 AA.

AAV44382;

14-MAR-2000 (first entry)

P. aeruginosa H coil-truncated K122 pilin protein.

KW Modified K122 pilin protein; alpha-helical forming portion;
 KW coiled coil homodimer; host cell-receptor site; *Pseudomonas* infection;
 KW cystic fibrosis; neutropenia.

OS *Pseudomonas aeruginosa*.

XX W09965511-A2.

XX 23-DEC-1999.

XX 11-JUN-1999; 99WO-CA00554.

XX 12-JUN-1998; 98US-0089155.

PA (UYAL-) UNIV ALBERTA.
 XX
 PI Hodges RS, Irvin RT;
 XX
 DR WPI: 2000-106013/09.
 DR N-PSDB; AA229541.
 XX
 PT Composition for treating or preventing *Pseudomonas aeruginosa* infection
 PT comprising pilin protein that can not self-assemble -
 XX
 PS Claim 1; Fig 4A; 32pp; English.

CC The present sequence is the H coil truncated K122 pilin protein from
 CC *P. aeruginosa*. The first 15-40 residues of the N-terminal peptide region
 CC is replaced by a peptide segment capable of forming a coiled-coil
 CC homodimer with an identical peptide segment which can form dimeric
 CC structures. These proteins are less inflammatory due to reduced degree of
 CC mobilisation of host-cell receptor sites. This prevents oligomerisation
 CC of pilin protein necessary for attachment to the host cell during
 CC infection. The modified pilin protein is useful in treatment and
 CC prophylaxis for individuals at risk of *Pseudomonas* infection,
 CC e.g. cystic fibrosis patients, burn patients, and severe neutropenic
 CC patients.

SO Sequence 175 AA;

Query Match 20.0%; Score 126; DB 21; Length 175;
 Best Local Similarity 29.3%; Pred. No. 3.5e-06;
 Matches 36; Conservative 17; Mismatches 60; Indels 10; Gaps 3;

QY 4 GTEFARSEGASALASVNP...LKTVEALSRGWSVKS...GTGTEADATKKEVPLG--VAADANKL 61
 Db 50 ggefaragqlsermtlasgltkvsdlfsgdscpantaatagiektdtinkkyavrtg 109
 QY 62 GTIALKPDPADGTADITLFTMGAGPKNKGIITLTFTAADG---LTKCTSDQDEQFIP 118
 Db 110 gtae-----assgctvalmkasdvatpigrkltlilgnadkgsylwactsnadnkyip 164
 QY 119 KGC 121
 Db 165 ktc 167

RESULT 12

AAAR38503
 ID AAR38503 standard; protein; 53 AA.

AAAR38503;

28-OCT-1993 (first entry)

P. aeruginosa pilin protein submolecular unit.

KW Antibodies; whole pilin binding; basis: vaccine; bacterial infection;
 KW ruminant footrot infection; sheep; type IV pillated bacteria.

OS *Pseudomonas aeruginosa*.

XX W09311791-A.

XX 24-JUN-1993.

XX 17-DEC-1992; 92WO-US11085.

XX 18-DEC-1991; 91US-0809762.

XX (UYOR-) UNIV OREGON HEALTH SCI.

XX Smith AW;

XX WPI; 1993-213824/26.

PT Antigenic preparation - stimulates production of antibodies binding
PT to pilin protein of type IV pillated bacteria, useful in
PT vaccine compsn.
XX
XX
PS Claim 18; Page 27; 44pp; English.
XX
CC The sequence is that of a submolecular unit of Pseudomonas aeruginosa
CC pilin protein which corresponds to at least one epitope common to
CC structural pilin proteins of type IV pillated bacteria. It is
CC capable of eliciting antibodies (Abs) which bind to whole pilli of
CC type IV bacteria. The ability of the submolecular unit to produce
CC Abs which bind to whole pilli provides the basis for vaccines against
CC type IV bacterial infections, e.g. footrot infection in ruminants.
XX
SQ Sequence 53 AA;

Query Match 16.9%; Score 106.5; DB 14; Length 53;
Best Local Similarity 96.2%; Pred. No. 0.0001;
Matches 25; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 8 ARSGSALASVNPDKTVEEALSRG 33
DB 29 arsegasal-svnpdkttveealsrg 53
|||||

RESULT 13
AAR25828
ID AAR25828 standard; Protein; 17 AA.
XX
AC AAR25828;
XX
DT 20-JAN-1993 (first entry)
XX
DE P. aeruginosa PAK mutant pilin C-terminal sequence.
XX
KW Strain PAK; Lys-to-Arg mutation; pulmonary epithelial cell.
XX
OS Pseudomonas aeruginosa.
XX
FH Key Location/Qualifiers
FH 7..13
FT Region /note= "peptides comprising at least this
FT antigenic subsequence are also claimed"
XX
XX W09212169-A.
XX
XX 23-JUL-1992.
XX
XX 24-DEC-1991; 91WO-CA00459.
XX
XX 04-JAN-1991; 91US-0638492.
XX
XX (SYNT-) SYNTHETIC PEPTIDES INC.
XX
XX Doig PC, Hodges RS, Irvin RT, Lee KK, Paranchych W;
XX Parimi SA, Wong WY, Zoutmon DE;
XX
XX WPI; 1992-268611/32.
XX
XX N-PSDB; AAQ26936.
XX
XX C-terminal portion of Pseudomonas aeruginosa pilin protein -
XX useful as a vaccine against non-Pseudomonas cross-reactive
XX microorganisms for preventing bacterial and fungal infections
XX
XX Claim 3(Amended); Page 72; 96pp; English.
XX
XX This sequence is the C-terminal amino acid sequence of pilin
XX from the P. aeruginosa strain PAK (Lys-to-Arg mutation), one of 10
XX strains which were investigated. The PAK (Lys-to-Arg mutation)
XX peptide is classified in a group with C-terminal peptides
XX containing 14 residues from Cys to Cys and is cross-reactive with
XX surface peptides in certain bacteria and fungi. The peptides bind

CC specifically to pulmonary epithelial cells.
CC See also AAR25900-R25908.
XX
SQ Sequence 17 AA;

Query Match 15.2%; Score 96; DB 13; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 107 KCTSDODEQFIPKGCGR 123
DB 1 kctsdqdegfipkgsck 17
|||||

RESULT 14
AAR25908
ID AAR25908 standard; peptide; 17 AA.
XX
AC AAR25908;
XX
DT 20-JAN-1993 (first entry)
XX
DE P. aeruginosa PAK pilin C-terminal sequence.
XX
KW Strain PAK; pulmonary epithelial cell.
XX
OS Pseudomonas aeruginosa.
XX
FH Key Location/Qualifiers
FH 7..13
FT Region /note= "peptides comprising at least this
FT antigenic subsequence are also claimed"
XX
XX W09212169-A.
XX
XX 23-JUL-1992.
XX
XX 24-DEC-1991; 91WO-CA00459.
XX
XX 04-JAN-1991; 91US-0638492.
XX
XX (SYNT-) SYNTHETIC PEPTIDES INC.
XX
XX Doig PC, Hodges RS, Irvin RT, Lee KK, Paranchych W;
XX Parimi SA, Wong WY, Zoutmon DE;
XX
XX WPI; 1992-268611/32.
XX
XX C-terminal portion of Pseudomonas aeruginosa pilin protein -
XX useful as a vaccine against non-Pseudomonas cross-reactive
XX microorganisms for preventing bacterial and fungal infections
XX
XX Claim 3(Amended); Page 72; 96pp; English.
XX
XX This sequence is the C-terminal amino acid sequence of pilin
XX from the P. aeruginosa strain PAK, one of 10 strains which were
XX investigated. The PAK peptide is classified in a group with
XX C-terminal peptides containing 14 residues from Cys to Cys and is
XX cross-reactive with surface peptides in certain bacteria and fungi.
XX The peptides bind specifically to pulmonary epithelial cells.
XX See also AAR25828 and AAR25900-R25907.
XX
XX Sequence 17 AA;

Query Match 14.7%; Score 93; DB 13; Length 17;
Best Local Similarity 94.1%; Pred. No. 0.00074;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 107 KCTSDODEQFIPKGCGR 123
DB 1 kctsdqdegfipkgsck 17
|||||

RESULT 15
AAD07E7E

ID	AA
AAK97575	standard; peptide; 17 AA.

AC AAR97575;

DT 19-JUL-1996 (first entry)
YY

DE	Mab PK99H antigen, PAK peptide.
XY	

KW Antigen; monoclonal antibody; Mab; PK99H; PAK plin protein; inhibition;
KW C-terminal receptor binding domain; combinatorial library set.

OS Synthetic.

FH	Key	Location/Qualifiers
FT	Peptide	7..13

FT	Peptide	7..13
----	---------	-------

/note= "epitope recognised by PK99H"

PN W09534575-A1.

PD 21-DEC-1995.

PF 13-JUN-1995; 95WO-IB00560.

PR 15-JUN-1994; 94US-0260199.

PA (SPIS-) SPI SYNTHETIC PEPTIDES INC.

PI Hodges RS, Holm A, Husband DL, Irvin RT, Sheth HB;
PI Wong WY;

DR WPI; 1996-049619/05.

PT Selecting oligomer, esp. peptide, for specific interaction with
PT macromolecular ligand - using sets of combinatorial oligomer
PT libraries with known residues at partic. positions, e.g. to identify
PT cpds which inhibit binding of pathogen to cellular receptor

PS Disclosure; Page 27; 61pp; English.

This sequence represents the antigen which is bound by the monoclonal antibody (MAb) PK99H. This peptide corresponds to a region of the C-terminal receptor binding domain of the PAK p11n protein. The peptides given in AAR97576-80 are members of combinatorial library sets which were screened for their ability to inhibit the interaction of PK99H with this antigen. The peptides given in AAR97576-79 showed a large inhibitory effect, whereas the peptide in AAR97580 shows a large loss of inhibitory effect. The peptides were prepared using the method of the invention which identifies optimum subunits for each position. This means that the number of permutation oligomers which have to be synthesised and tested for optimal activity is fairly low.

Sequence 17 AA;

Query Match	14.78;	Score 93;	DB 17;	Length 17;
PostgreSQL	0.18	0.18	0.18	0.18

Best Local Similarity 94.18; Pred. No. 0.00074;
Matches 16; Conservation 1

Matches	16;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;
---------	-----	--------------	----	------------	----	--------	----	------	----

```

OY      107 KCTSDQDEQFIPKCSR 123
          |||||
Db       1 kctsdqdeqfipkcsk 17

```


GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Inc.

OM protein - protein search, using sw model

Run on: February 8, 2002, 15:23:15 ; Search time 37.87 Seconds

(without alignments)
247.411 Million cell updates/sec

Title: US-09-865-159-4

Perfect score: 631
Sequence: 1 ALEGTGFARSEGASALASLVN.....GLMCTSDQDEQFIRKGCGR 123

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	593	94.0	150	1 YQPSA	fimbrial protein p
2	301.5	47.8	149	2 A25023	type 4 fimbrial pr
3	294.5	46.7	150	2 A43504	pilin precursor -
4	285.5	45.2	150	2 B24603	fimbrial protein -
5	126.5	20.0	136	2 S52692	fimbriillin - xanth
6	111	17.6	157	2 A31105	fimbrial protein p
7	110.5	17.5	156	2 S15267	fima protein - Dic
8	109.5	17.4	167	2 G82077	fimbrial protein v
9	109	17.3	148	2 F82544	fimbrial protein x
10	108.5	17.2	136	2 D36961	pilin pilA precurs
11	105.5	16.7	164	2 A42460	fimbrial protein q
12	102.5	16.2	157	2 A24434	beta fimbrial prot
13	99.5	15.8	154	2 S04440	fimbrial protein -
14	99.5	15.8	154	2 B31105	fimbrial protein p
15	99	15.7	148	2 C82544	fimbrial protein x
16	98.5	15.6	159	1 YQBNH2	fimbrial protein f
17	93.5	14.8	159	1 YQBNH2	fimbrial protein f
18	91	14.4	155	2 JU0711	alpha-pilin - Mora
19	89	14.1	160	2 A37167	pilin precursor -
20	89	14.1	350	2 F86804	basic membrane pro
21	87.5	13.9	159	2 A47699	type 4 pilin - Eik
22	87	13.8	218	2 T28689	hypothetical prote
23	86.5	13.7	1128	1 T08312	plasmid replicatio
24	86	13.6	156	2 S15266	fima protein - Dic
25	86	13.6	157	2 A46566	pilin precursor -
26	85.5	13.5	156	2 A41490	pilin precursor -
27	84	13.3	3588	2 A40485	surfactin syntheta
28	82.5	13.1	252	2 S50806	hypothetical prote
29	80	12.7	385	2 T35516	hypothetical prote

30	80	12.7	1485	1 TS2PT2	DNA topoisomerase
31	79.5	12.6	158	2 S15263	fima protein - Dic
32	79.5	12.6	539	2 T50579	probable membrane
33	79.5	12.6	856	2 T00349	Avicelase III - As
34	78.5	12.4	135	2 S52693	fimbriillin - Xanth
35	78	12.4	161	2 S15262	fima protein - Dic
36	77.5	12.3	158	2 A55851	prepilin - Moraxel
37	77	12.2	515	2 H72455	hypothetical prote
38	76.5	12.1	94	2 T37166	hypothetical prote
39	76.5	12.1	474	2 T27297	hypothetical prote
40	76	12.0	186	2 C82794	fimbriillin xF0538
41	75.5	12.0	327	2 A72390	hypothetical prote
42	74.5	11.8	1677	2 T18344	p-glycoprotein E -
43	74.5	11.6	231	2 T31315	hypothetical prote
44	73.5	11.6	243	2 S58494	auxin-induced prote
45	73.5	11.6	408	2 T16601	hypothetical prote

ALIGNMENTS

RESULT 1

YQPSA

fimbrial protein precursor - Pseudomonas aeruginosa (strain PAK)

N:Alternate names: pilin

C:Species: Pseudomonas aeruginosa

C>Date: 14-Nov-1983 #sequence_revision 16-Oct-1998 #text_change 16-Jul-1999

C/Accession: A24603; A28780; A03497

R:Johnson, K.; Parker, M.L.; Lory, S.

J. Biol. Chem. 261, 15703-15708, 1986

A>Title: Nucleotide sequence and transcriptional initiation site of two Pseudomonas

A/Reference number: A24603; MUID:87057209

A/Accession: A24603

A/Molecule type: DNA

A/Residues: 1-150 <J0H>

A/Cross-references: GB:M14849; GB:J02609; NID:q151479; PIDN:AA25955.1; PID:q151480

R:Pasloske, B.L.; Finlay, B.B.; Paranchych, W.

FEBS Lett. 183, 408-412, 1985

A>Title: Cloning and sequencing of the Pseudomonas aeruginosa PAK pilin gene.

A/Reference number: A28780; MUID:85180008

A/Accession: A28780

A/Molecule type: DNA

A/Residues: 1-149, 'R' <PSK>

A/Cross-references: GB:X02402; GB:M11462; NID:q45331; PIDN:CAA26248.1; PID:q45332

R:Sastiy, P.A.; Pearlstone, J.R.; Smillie, L.B.; Paranchych, W.

FEBS Lett. 151, 253-256, 1983

A>Title: Amino acid sequence of pilin isolated from Pseudomonas aeruginosa PAK.

A/Reference number: A03497; MUID:83158129

A/Accession: A03497

A/Molecule type: protein

A/Residues: 7-90, 'S', '91-100', 'DTA', '104-150' <SAS>

A/Note: the pilin from which this protein was isolated are polar flexible filaments o

C:Superfamily: gonococcal fimbrial protein

C/Keywords: fimbria; methylated amino end; pilin formation

F:1-6/Domain: propeptide #status predicted <PRO>

F:7-150/Product: fimbrial protein #status predicted <MAT>

F:7/Modified site: methylated amino end (Phe) (in mature form) #status predicted

Query Match Score 593; DB 1; Length 150;

Best Local Similarity 99.1%; Pred. No. 4e-49;

Matches 115; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 8 ARSEGASALASVNPDKTVEEALSRGMSVSGTGTEDATKKEVPLGVAAADANKLTGTTALK 67

DB 35 ARSEGASALASVNPDKTVEEALSRGMSVSGTGTEDATKKEVPLGVAAADANKLTGTTALK 94

OY 68 PDADGTADITLFTTGGAGPRKNGKITTITRTAADGLMCTSDQDEQFIRKGCGR 123

DB 95 PDADGTADITLFTTGGAGPRKNGKITTITRTAADGLMCTSDQDEQFIRKGCGR 150

RESULT 2

A25023

Type 4 fimbrial precursor PIIA PA4525 [imported] - Pseudomonas aeruginosa (strain PA01)

N:Alternate names: Piliin

C:Species: Pseudomonas aeruginosa

C>Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 31-Dec-2000

C:Accession: A25023; H83080

R:Sastry, P.A.; Finlay, B.B.; Pasloske, B.L.; Paranchych, W.; Pearlstone, J.R.; Smillie, J. Bacteriol. 164, 571-577, 1985

A:Title: Comparative studies of the amino acid and nucleotide sequences of piliin derived

A:Reference number: A25023; MUID:86033611

A:Accession: A25023

A:Molecule type: DNA

A:Residues: 1-149 <SAS>

A:Cross-references: GB:M11323; NID:g151477; PIDN:AAA25954.1; PID:g151478

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Berman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, N.; Lory, S.; Olson, M.V.

Nucleotide: 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho

A:Reference number: A82950; MUID:20437337

A:Accession: H83080

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-149 <STO>

A:Cross-references: GB:AE004866; GB:AE004091; NID:g9950760; PIDN:AG07913.1; GSPDB:GN001

A:Experimental source: strain PA01

C:Genetics:

A:Gene: PIIA: PA4525

C:Superfamily: gonococcal fimbrial protein

C:Keywords: methylated amino end

F:7/Modified site: methylated amino end (Phe) (in mature form) #status predicted

Query Match

47.8%; Score 301.5; DB 2; Length 149;

Best Local Similarity 58.1%; Pred. No. 1.5e-21;

Matches 68; Conservative 12; Mismatches 30; Indels 7; Gaps 4;

Db 35 ARSEGASALATINPLKTTVEESLSRGIAISKIKIGTASTAT--ETVVGVEPPDNKLGVI 92

QY 8 ARSEGASALASVNPDKTVEEALSRGMS--VKSQTGEDATKKEVPLGVAADANKIGTAL 64

Db 65 ALKEDPADGTADITLFTMGAGAPKNGKIIITLRTAADGLMKTSDODQFIPKGC 121

Db 93 AVAIEDS-GAGDITFTQTGTSPKRNATKYITLNR--ADGVWACKSTQDPEFIPKGC 147

RESULT 3

A43504

Piliin precursor - Pseudomonas aeruginosa

C:Species: Pseudomonas aeruginosa

C>Date: 21-Oct-1992 #sequence_revision 21-Oct-1992 #text_change 29-Jan-1999

C:Accession: A43504

R:Pasloske, B.L.; Joffe, A.M.; Sun, Q.; Voipel, K.; Paranchych, W.; Eftekhari, F.; Speert

A:Title: Serial isolates of Pseudomonas aeruginosa from a cystic fibrosis patient have

A:Reference number: A43504; MUID:88138467

A:Accession: A43504

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-150 <PAS>

A:Cross-references: GB:M24281

C:Superfamily: gonococcal fimbrial protein

C:Keywords: methylated amino end

F:7/Modified site: methylated amino end (Phe) (in mature form) #status predicted

Query Match

46.7%; Score 294.5; DB 2; Length 149;

Best Local Similarity 55.9%; Pred. No. 7.2e-21;

Matches 66; Conservative 16; Mismatches 31; Indels 4;

Db 8 ARSEGASALASVNPDKTVEEALSRGMS--VKSQTGEDATKKEVPLGVAADANKIGTAL 64

QY 8 ARSEGASALASVNPDKTVEEALSRGMS--VKSQTGEDATKKEVPLGVAADANKIGTAL 64

Db 35 ARSEGASALATINPLKTTVEESLSRGIAISKIKIGTASTADTTYVGVDEKANKIGTAAV 94

QY 67 K-PPADGTADITLFTMGAGAPKNGKIIITLRTAADGLMKTSDODQFIPKGC 123

Db 95 TIKDTGDT--VKTFPATGSSPKRNAGKEITLNR--AEVWCTSTQDEMFIPKGC 149

RESULT 4

B24603

Fimbrial protein - Pseudomonas aeruginosa (strain PA103)

C:Species: Pseudomonas aeruginosa

C>Date: 11-Dec-1987 #sequence_revision 11-Dec-1987 #text_change 26-Aug-1999

C:Accession: B24603

R:Johnson, K.; Parker, M.L.; Lory, S.

J. Biol. Chem. 261, 15703-15708, 1986

A:Title: Nucleotide sequence and transcriptional initiation site of two Pseudomonas

A:Reference number: A24603; MUID:87057209

A:Accession: B24603

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-150 <JOH>

A:Cross-references: GB:M14850; GB:J02609; GB:J02682; NID:g151475; PIDN:AAA25953.1; P

C:Superfamily: gonococcal fimbrial protein

C:Keywords: methylated amino end

F:7/Modified site: methylated amino end (Phe) (in mature form) #status predicted

Query Match

45.2%; Score 285.5; DB 2; Length 150;

Best Local Similarity 55.6%; Pred. No. 5.1e-20;

Matches 65; Conservative 15; Mismatches 32; Indels 5; Gaps 4;

Db 35 ARSEGASALATINPLKTTVEESLSRGIAISKIKIGTASTADTTYVGVDEKANKIGTAAV 94

QY 8 ARSEGASALASVNPDKTVEEALSRGMS--VKSQTGEDATKKEVPLGVAADANKIGTAL 66

Db 67 K-PPADGTADITLFTMGAGAPKNGKIIITLRTAADGLMKTSDODQFIPKGC 122

Db 95 TIKDTGDT--IKFNATGSSPKRNAGKEITLNR--AEVWCTSTQDEMFIPKGC 148

RESULT 5

S52692

Fimbriillin - Xanthomonas campestris

C:Species: Xanthomonas campestris

C>Date: 19-May-1995 #sequence_revision 01-Sep-1995 #text_change 24-Nov-1999

C:Accession: S52692

R:Ojane, T.M.; Kalkkinen, N.; Westerlund, B.; van Doorn, J.; Hahtela, K.; Korhonen,

submitted to the EMBL Data Library, March 1995

A:Description: Characterization of the fimb gene encoding the type IV fimbriillin of t

A:Reference number: S52692

A:Accession: S52692

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-136 <OJA>

A:Cross-references: EMBL:Z48759; NID:g747907; PIDN:CA88680.1; PID:g747908

C:Superfamily: gonococcal fimbrial protein

Query Match

20.0%; Score 126.5; DB 2; Length 136;

Best Local Similarity 32.5%; Pred. No. 5.1e-05;

Matches 37; Conservative 18; Mismatches 44; Indels 15; Gaps 4;

QY 8 ARSEGASALASVNPDKTVEEALSRGMS--VKSQTGEDATKKEVPLGVAADANKIGTAL 67

Db 35 AKSQVTAGLAETNPKGTQYVALNEG---KTVADTTE---LGKSPSEKTIAPIT 85

QY 68 PDPADGTADITLFTMGAGAPKNGKIIITLRTAADGLMKTSDODQFIPKGC 121

Db 86 ALSAGTIECTLK-----GNTQVGGKATYTLR--ANDGWCTKTDALKKYPAGC 133

RESULT 6

A31105

fimbrial protein precursor - *Pseudomonas aeruginosa* (strain K12-4)

C:Species: *Pseudomonas aeruginosa*

C>Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 26-Aug-1999

C:Accession: A31105

R:Pasloske, B.L.; Sastry, P.A.; Finlay, B.B.; Paranchych, W.

J: Bacteriol. 170, 3738-3741, 1988

A:Title: Two unusual pilin sequences from different isolates of *Pseudomonas aeruginosa*.

A:Reference number: A91879; MUID:88298689

A:Accession: A31105

A:Molecule type: DNA

A:Residues: 1-157 <PAS>

A:Cross-references: GB:M21651; NID:9151473; PIDN:AC63062.1; PID:9151474

C:Superfamily: gonococcal fimbrial protein

C:Keywords: methylated amino end

F:1-7/Domain: propeptide #status predicted <PRO>

F:8-157/Product: fimbrial protein #status predicted <MAP>

F:8/Modified site: methylated amino end (Phe) (in mature form) #status predicted

Query Match 17.6%; Score 111; DB 2; Length 157;

Best Local Similarity 27.7%; Pred. No. 0.0018;

Matches 33; Conservative 17; Mismatches 59; Indels 10; Gaps 3;

OY 8 ARSEGASALASVNPDKTVEEALSRGWSVKSCTGTEADATKKEVPLG--VAADANKLGTIA 65

DB 36 ARAQLSERMTLASGLKTKYSDIFSGDSCPANTATAGIEKTDINGKVKVTTGCTAA 95

OY 66 LKPPADGTAADTLTFTMGAGAPKAKKIITLTAAAG--LWKCTSDDEQIFPKCC 121

DB 96 ---ASGCTIVATMKASDVATPLRKTITLTLCNADKGSYVACTSNADNKYLPKTC 149

RESULT 7

fima protein - *Dichelobacter nodosus*

C:Species: *Dichelobacter nodosus*

C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 26-Aug-1999

C:Accession: S15267

R:Matlick, J.S.; Anderson, B.J.; Cox, P.T.; Dalrymple, B.P.; Bills, M.W.; Hobbs, M.; Egg

MOL. Microbiol. 5, 561-573, 1991

A:Title: Gene sequences and comparison of the fimbrial subunits representative of *Bacter*

A:Reference number: S15258; MUID:91260440

A:Accession: S15267

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-156 <MAP>

A:Cross-references: EMBL:X52390; NID:939703; PIDN:CA36619.1; PID:939704

C:Superfamily: gonococcal fimbrial protein

C:Keywords: methylated amino end

F:8/Modified site: methylated amino end (Phe) (in mature form) #status predicted

Query Match 17.5%; Score 110.5; DB 2; Length 156;

Best Local Similarity 23.4%; Pred. No. 0.002;

Matches 34; Conservative 22; Mismatches 36; Indels 53; Gaps 6;

OY 8 ARSEGASALASVNPDKTVEEALSR-----GMSVKS-----GNGTADATKKEVPL 52

DB 36 ARSQVSRVMTSGMRTAIEICLDGKRGKCFIGWTISNLLAAGSSTNNATAE----- 91

OY 53 GVAADANKLGTIALKPPADGTAADTLTFTMGAGAPKAK-----GKIITLT 98

DB 92 -----PBGQGLNTIYAL--GSTAEKRIATFGQNAATLHGKXKLWT 132

OY 99 RTAADGLMKCTSDDEQIFPKCSR 123

DB 133 R-SPEATWSCSTDVDEKFKPTGCKO 156

RESULT 8

fimbrial protein VC2423 (imported) - *Vibrio cholerae* (strain N16961 serogroup O1)

C:Species: *Vibrio cholerae*

C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001

C:Accession: G82077

R:Heidelberg, J.F.; Eissen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R

Charidson, D.; Ermolaeva, M.D.; Vamathavan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellar

1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A:Title: DNA sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.

A:Reference number: A82035; MUID:20406833

A:Accession: G82077

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-167 <HEP>

A:Cross-references: GB:AE004312; GB:AE003852; NID:9656995; PIDN:AAE95566.1; GSPDB:G

A:Experimental source: serogroup O1; strain N16961; biotype El Tor

C:Genetics:

A:Gene: VC2423

A:Map position: 1

C:Superfamily: gonococcal fimbrial protein

Query Match 17.4%; Score 109.5; DB 2; Length 167;

Best Local Similarity 31.0%; Pred. No. 0.0026;

Matches 36; Conservative 17; Mismatches 38; Indels 25; Gaps 6;

OY 16 LASVNPDKTVEEALSRGWSVKSCTGTEADATKKEVPLGVAADANKLGTIALKPPADGTA 75

DB 62 LANITALKNTIEDYATGSEPPATTA-----GTAAETRLGTV---EDMGDKI 107

OY 76 DI--TLFTMGG-----AGPKNKGIITLTAAAGLMTKTSDDDEQIFPKCS 122

DB 108 VIAPASGALGTTIYRTDAGVSSK--IQIARD--ANGLMCTSTVTSIAPKCT 161

RESULT 9

fimbrial protein XF2542 (imported) - *Xylella fastidiosa* (strain 9a5c)

C:Species: *Xylella fastidiosa*

C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000

C:Accession: F82544

R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Se

Nature 406, 151-157, 2000

A:Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.

A:Reference number: A82515; MUID:20365717

A>Note: for a complete list of authors see reference number A59328 below

A:Accession: F82544

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-148 <SIM>

A:Cross-references: GB:AE004061; GB:AE003849; NID:9107747; PIDN:AAE85339.1; GSPDB:G

A:Experimental source: strain 9a5c

R:Simson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R

Bridões, M.R.S.; Bueno, M.R.P.; Camargo, L.E.A.; Carraro, D.M.; Carre

as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to Genbank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; F

J.D.; Junqueira, M.L.; Kemp, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; L

chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Martino, C.L.; Marques, M.V.; Martin

A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C

, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri,

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Saw

A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Sil

M.; Tsubako, M.H.; Valada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L

A:Reference number: A59328

A:Contents: annotation

C:Genetics:

A:Gene: XF2542

C:Superfamily: gonococcal fimbrial protein

Query Match 17.3%; Score 109; DB 2; Length 148;

Best Local Similarity 29.6%; Pred. No. 0.0025;

Matches 37; Conservative 15; Mismatches 49; Indels 24; Gaps 4;

```

Best Local Similarity 30.5%; Pred. No. 0.0062;
Matches 39; Conservative 20; Mismatches 54; Indels 15; Gaps 6;

QY 8 ARSEGASALASVNPILKTTVEEALSRGWSVKSTGTEDATFKREVPV---GVAADANKL--- 61
      :::      :      :      :      :      :      :      :      :      :      :
Db 35 SKSOTTRRVAGELAGAKTAVDALFEGRKEPVLDAAGTATATSKEDIGLTSTGKARSNLLKET 94
      :      :      :      :      :      :      :      :      :      :
QY 62 GTIALKPDPADGTADITLFTFTMGAGAPRN-KGRITTLTFTAADGLMKCTSDQ-----DE 114
      |      |      |      |      |      |      |      |      |      |
Db 95 GGVVLAGSASNSAG-TITGTGLNRRANKDISCAITTKR-ANDGVWTCVQOQGTATGWRKD 152
      :      :      :      :      :      :      :      :      :      :
QY 115 QPIRKGS 122
      :      :      :      :      :      :      :      :      :      :
Db 153 KEIPIGCT 160

RESULT 12
A24434
beta fimbrial protein precursor - Moraxella bovis
N:Alternate names: beta pilin
C:Species: Moraxella bovis
C:Date: 08-Aug-1987 #sequence_revision 08-Aug-1987 #text_change 26-Aug-1999
C:Accession: A24434; J010072
R:Marrs, C.F.; Schoolnik, G.; Koomey, J.M.; Hardy, J.; Rothbard, J.; Falkow, S.
J. Bacteriol. 163, 132-139, 1985
A:Reference number: A24434; MUID:85234350
A:Accession: A24434
A:Molecule type: DNA
A:Residues: 1-157 <MAR>
A:Cross-references: GM:11435; NID:g149760; PIDN:AAA25304.1; PID:g149761
A:Experimental source: strain EPP63
A:Publ W W: Marrs, C F.; Fernandez, R.; Falkow, S.; Schoolnik, G.K.

```

```

A:Title: Purification, characterization, and pathogenicity of Moraxella dovis pili
A:Reference number: J10071; MUID:89010522
A:Accession: J10072
A:Molecule type: protein
A:Residues: 786,93-122 <RUE>
A:Note: about 50% of the amino-terminus is N-methylated; the remaining 50% of the m
C:Superfamily: gonococcal fimbrial protein
C:Keywords: methylated amino end; surface antigen
F:1-6/Domain: propeptide #status predicted <PRO>
F:7-157/Product: beta fimbrial protein 1 #status experimental <MA2>
F:8-157/Product: beta fimbrial protein 2 #status experimental <MA2>
F:7/Modified site: methylated amino end (Phe) (in mature form) #status experimental
F:136-135/Disulfide bonds: #status experimental

Query Match          16.2%; Score 102.5; DB 2; Length 157;
Best Local Similarity 28.2%; Pred. No. 0.011;
Matches 35; Conservative 25; Mismatches 51; Indels 13; Gaps 6;

QY      8 ARSEGAALASVNP LKTYVEALSRGVSXSGTGTEDAKKEVPL---GYAADANKIGTI 64
      :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
Db      35 SKSQTRRVVGEALAGACTAVDAALFECKTRPLGLGAAND-DEEDIGLTTTGGTARSNIMSSV 93

QY      65 AKPPADGTDADITLFTFTMGAGAPKN-KGKIIFRFLTAADGLMKCTSDQD-----EQFI 117
      :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
Db      94 NI-GGCAFEFTGAGTLEATLGNRANKRIDIAGAVITQSD-AGVWTCITINGSAAPGWRKSKFV 151

QY      118 PKGC 121
      |||
Db      152 PRGC 155

RESULT 13
S04440
fimbrial protein - Pseudomonas aeruginosa (strain 1244)
N:Alternate names: pilin
C:Species: Pseudomonas aeruginosa
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 26-Aug-1999
C:Accession: S04440
R:Castiric, P.A.; Sidberry, H.F.; Sadoff, J.C.

```

Mol. Gen. Genet. 216, 75-80, 1989

A:Title: Cloning and sequencing of the *Pseudomonas aeruginosa* 1244 pilin structural gene

A:Reference number: S04440; MUID:89281493

A:Accession: S04440

A>Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-154 <CAS>

C:Superfamily: gonococcal fimbrial protein

Query Match 15.8% Score 99.5; DB 2; Length 154;

Best Local Similarity 27.6%; Pred. No. 0.021; Mismatches 51; Indels 19; Gaps 7;

Matches 35; Conservative 22; Mismatches 51; Indels 19; Gaps 7;

Y 8 ARSEGASALASVNPDKTVEEALSRGMSVKSCTGTEADATKEVPLGVAADANKL-----GT 63

DB 35 ARQVTRAVSEVSAKTAESAILEGKEIVS-----SATPKDQYDIDIFESTLIDSGK 89

Y 64 IALK-PDPAQGTADITLFTMG-GAGPKNKGIITLTPTAADGLMKTSDO-----DEQF 116

DB 90 SQIQVTDNQDGT--VELVATLGKSSGSAIKGAVITVSR-KNDGVWNCIKITPTAKPKNY 146

Y 117 IPKGCGR 123

DB 147 APANCPK 153

RESULT 14

B31105 fimbrial protein precursor - *Pseudomonas aeruginosa* (strain P1)

C:Species: *Pseudomonas aeruginosa*

C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 08-Oct-1999

C:Accession: B31105

J:Paolozze, B.B.; Sastry, P.A.; Finlay, B.B.; Paranchych, W.

J:Paolozze, B.B.; Sastry, P.A.; Finlay, B.B.; Paranchych, W.

A:Title: Two unusual pilin sequences from different isolates of *Pseudomonas aeruginosa*.

A:Reference number: A91879; MUID:88298689

A:Accession: B31105

A:Molecule type: DNA

A:Residues: 1-154 <PPAS>

A:Cross-references: GB:M21652; NID:g151471; PIDN:AA63060.1; PID:g151472

C:Superfamily: gonococcal fimbrial protein

F:1-6/Domain: signal sequence #status predicted <SIG>

F:7-154/Product: fimbrial protein #status predicted <MAT>

Query Match 15.8% Score 99.5; DB 2; Length 154;

Best Local Similarity 27.6%; Pred. No. 0.021; Mismatches 51; Indels 19; Gaps 7;

Matches 35; Conservative 22; Mismatches 51; Indels 19; Gaps 7;

Y 8 ARSEGASALASVNPDKTVEEALSRGMSVKSCTGTEADATKEVPLGVAADANKL-----GT 63

DB 35 ARQVTRAVSEVSAKTAESAILEGKEIVS-----SATPKDQYDIDIFESTLIDSGK 89

Y 64 IALK-PDPAQGTADITLFTMG-GAGPKNKGIITLTPTAADGLMKTSDO-----DEQF 116

DB 90 SQIQVTDNQDGT--VELVATLGKSSGSAIKGAVITVSR-KNDGVWNCIKITPTAKPKNY 146

Y 117 IPKGCGR 123

DB 147 APANCPK 153

RESULT 15

C82544

fimbrial protein XF2539, [imported] - *Xylella fastidiosa* (strain 9asc)

C:Species: *Xylella fastidiosa*

C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000

C:Accession: C82544

R:Anonymous, The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Sequen

Nature 406, 151-157, 2000

A:Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.

A:Reference number: A82515; MUID:20365717

A>Note: for a complete list of authors see reference number A59328 below

A:Accession: C82544

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-148 <STM>

A:Cross-references: GB:AE004061; GB:AE003849; NID:g9107747; PIDN:AAE85336.1; GSPDB:G

A:Experimental source: strain 9asc

R:Simpson, A.J.G.; Reinach, F.C.; Artuda, P.; Abreu, F.A.; Acencio, M.; Alvares, R

Brienes, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carre

as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to Genbank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franco, S.C.; Franco, M.C.; F

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; L

chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Marti

A:Authors: Martins, E.M.F.; Matsushima, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C

F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri,

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sav

A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Sil

M.; Tsunako, M.H.; Valisda, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L

A:Reference number: A59328

A:Contents: annotation

C:Genetics:

A:Gene: XF2539

C:Superfamily: gonococcal fimbrial protein

Query Match 15.7% Score 99; DB 2; Length 148;

Best Local Similarity 29.8%; Pred. No. 0.023; Mismatches 39; Conservative 16; Mismatches 38; Indels 38; Gaps 8;

Matches 39; Conservative 16; Mismatches 38; Indels 38; Gaps 8;

Y 8 ARSEGASALASVNPDKTVEEALSRGMSVKSCTGTEADATKEVPLGVAADANKLGTALK 67

DB 35 ARSOLTAALADITPGKVAESLIADG-----KSTNSASD-----IGLRTDTTRCG-ITVK 83

Y 68 PDPAQGTADITLFTMGAGAPKNGK-----KITLTPTAAD-----GLMKTSD 111

DB 84 VDAA-GTANITC-----KVGNSQVNDKTAMRTSDNSAGTNGVNGGWTGCSST 133

Y 112 -QDEQFIPKGC 121

DB 134 VTSALPSPGC 144

Search completed: February 8, 2002, 15:25:55

Job time: 160 sec

Fri Feb 8 15:44:51 2002

us-09-865-159-4.rpt

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 8, 2002, 15:25:15 ; Search time 22.14 Seconds

(without alignments)
203.693 Million cell updates/sec

Title: US-09-865-159-4

Sequence: 1 ALEGTFFAFSEGAALASVYN.....GLMKCTSDODEQIFPKGCSR 123

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	596	94.5	150 1	FMPA_PSEAE
2	301.5	47.8	149 1	FMPD_PSEAE
3	294.5	46.7	150 1	FMPD_PSEAE
4	285.5	45.2	150 1	FMPD_PSEAE
5	115.5	18.3	156 1	FMAH_BACNO
6	111	17.6	157 1	FMPD_PSEAE
7	108.5	17.2	136 1	FMPD_PSEAE
8	102.5	16.2	157 1	FMO_MORBO
9	99.5	15.8	154 1	FMPD_PSEAE
10	99.5	15.8	154 1	FMPD_PSEAE
11	98.5	15.6	159 1	FMPD_PSEAE
12	93.5	14.8	159 1	FMPD_PSEAE
13	92.5	14.7	153 1	ECPC_EIKCO
14	91	14.4	159 1	FMI_MORBO
15	89	14.1	160 1	FMAJ_BACNO
16	87.5	13.9	159 1	ECPC_EIKCO
17	86	13.6	156 1	FMAJ_BACNO
18	84	13.3	3587 1	SRR1_BACSU
19	82.5	13.1	252 1	YUG6_YEAST
20	80	12.7	1485 1	TOP2_SCHPO
21	79.5	12.6	158 1	FMAF_BACNO
22	78	12.4	161 1	FMAF_BACNO
23	73.5	11.6	243 1	AKT7_ARATH
24	72.5	11.5	2769 1	THYG_BOVIN
25	72	11.4	236 1	AXIG_ARATH
26	71	11.3	161 1	FMAJ_BACNO
27	71	11.3	442 1	SPO3_MOUSE
28	69.5	11.0	523 1	PEO_LISSE
29	68.5	10.9	152 1	ECPC_EIKCO
30	68.5	10.9	159 1	ECPC_EIKCO
31	68	10.8	337 1	TRPD_BRAVA
32	68	10.8	344 1	YD33_MYCTU
33	68	10.8	461 1	KLB2_ECOLI

ALIGNMENTS

RESULT	ID	FMPP_PSEAE	STANDARD	PRT	150 AA
34	68	10.8	623	1	DNK_CYAPA
35	68	10.8	680	1	GAOA_DACE
36	68	10.8	683	1	AMPH_RAT
37	67.5	10.7	250	1	H1L_DROVI
38	67.5	10.7	257	1	MADE_PYRHO
39	67	10.6	480	1	TGNS_HUMAN
40	67	10.6	670	1	GR78_YARLI
41	67	10.6	752	1	CAT1_MYCO
42	67	10.6	1179	1	ATX1_ARATH
43	67	10.6	1181	1	SCA2_STRPY
44	67	10.6	1786	1	UVRA_CHLTR
45	66.5	10.5	338	1	AXI9_ARATH

FMPP_PSEAE	1	FMPP_PSEAE	STANDARD	PRT	150 AA
AC	P02973; Q53390;				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	01-NOV-1990 (Rel. 16, Last sequence update)				
DT	01-NOV-1997 (Rel. 35, Last annotation update)				
DE	FIBRIL PROTEIN PRECURSOR (PILIN) (STRAIN PAK).				
GN	PILA OR FIWA.				
OS	Pseudomonas aeruginosa.				
OC	Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;				
CC	Pseudomonas.				
OX	NCBI_TaxID=287;				
RN	[1]				
RC	SEQUENCE FROM N.A.				
RP	STRAIN-PAK;				
RX	MEDLINE=87057209; PubMed=2430961;				
RA	Sasstry P.A., Pearlstone J.R., Smillie L.B., Paranchych W.;				
RT	"Amino acid sequence of pilin isolated from Pseudomonas aeruginosa PAK pilin				
RL	gene.";				
RL	FEBS Lett. 183:408-412(1985).				
RN	[2]				
RC	SEQUENCE FROM N.A.				
RP	STRAIN-PAK;				
RX	MEDLINE=87057209; PubMed=2430961;				
RA	Johnson K., Parker M.L., Lory S.;				
RT	"Nucleotide sequence and transcriptional initiation site of two				
RL	Pseudomonas aeruginosa pilin genes.";				
RN	J. Biol. Chem. 261:15703-15708(1986).				
RN	[3]				
RC	SEQUENCE OF 7-150.				
RX	STRAIN-PAK;				
RA	MEDLINE=83158129; PubMed=6131838;				
RT	Sasstry P.A., Pearlstone J.R., Smillie L.B., Paranchych W.;				
RL	"Amino acid sequence of pilin isolated from Pseudomonas aeruginosa				
RL	PAK.";				
RL	FEBS Lett. 151:253-256(1983).				
RN	[4]				
RC	SEQUENCE OF 128-150 FROM N.A.				
RX	MEDLINE=94103636; PubMed=7903973;				
RA	IPATSG;				
RT	"A multicenter comparison of methods for typing strains of				
RL	Pseudomonas aeruginosa predominantly from patients with cystic				
RT	fibrosis. The International Pseudomonas aeruginosa Typing Study				
RT	Group.";				
RL	J. Infect. Dis. 169:134-142(1994).				
RN	[5]				
RC	STRUCTURE BY NMR OF 134-150.				
RX	MEDLINE=94079874; PubMed=8257679;				
RA	McInnes C., Seemichsen F.D., Kay C.M., Hodges R.S., Sykes B.D.;				
RT	"NMR solution structure and flexibility of a peptide antigen				
RL	representing the receptor binding domain of Pseudomonas aeruginosa.";				
CC	Biochemistry 32:13432-13440(1993).				
CC	-I- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4				
CC	NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY				
CC	CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL				

CC CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.
CC -1- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL: M14849; AAA25955.1;
DR EMBL: X02402; CAA26248.1;
DR EMBL: S67807; CAB32859.1;
DR PIR: A03497; YOPSPA.
DR PIR: A24603; A24603.
DR PIR: A28780; A28780.
DR PDB: 1PAJ; 31-JAN-94.
DR PDB: 1PAJ; 31-JAN-94.
DR PDB: 1N1L; 29-JAN-96.
DR PDB: 1N1L; 29-JAN-96.
DR InterPro: IPR001082; PiliN.
DR InterPro: IPR001120; Prok_N_methyln.
DR Pfam: PF00114; PiliN; 1.
DR ProDom: PD000666; PiliN; 1.
DR PROSITE: PS00409; PROKAR_NTER_METHYL; 1.
KW Fimbria; Methylation; 3D-structure.
FT PROPEP 1 6
FT CHAIN 1 150
FT MOD_RES 7 150 FIMBRIAL PROTEIN.
FT DISULFID 135 148 METHYLATION (BY SIMILARITY).
FT CONFLICT 90 90
FT CONFLICT 101 103 T -> TS (IN REF. 3).
FT CONFLICT 128 128 TAD -> DTA (IN REF. 3).
FT CONFLICT 150 150 A -> D (IN REF. 4).
FT CONFLICT 150 150 R -> K (IN REF. 2).
SQ SEQUENCE 150 AA; 15650 MW; COE35B69DF6FBE84 CRC64;

Query Match 94.5%; Score 596; DB 1; Length 150;
Best Local Similarity 100.0%; Pred. No. 1.1e-47;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 ARSEGASALASVNPDKTYEALSRGWSYKSGTGDATKKEVPLGVADANKLGTIAIK 67
DB 35 ARSEGASALASVNPDKTYEALSRGWSYKSGTGDATKKEVPLGVADANKLGTIAIK 94
QY 68 PDPADGTADITLFTWGMGAGPRNKGKIIITLRTADGLMKCTSDDEQFIPKGCGR 123
DB 95 PDPADGTADITLFTWGMGAGPRNKGKIIITLRTADGLMKCTSDDEQFIPKGCGR 150

RESULT 2
FMPO_PSEAE STANDARD: PRT; 149 AA.
AC P04739;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE FIMBRIAL PROTEIN PRECURSOR (PILIN) (STRAIN PAO).
GN PILA OR PTMA OR PA4525.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PAO;
RX MEDLINE=86033611; PubMed=2997119;
RA Sastiy P.A., Finlay B.B., Pasloske B.L., Paranchych W.,
RA Pearlstone J.R., Smillie L.B.;
RT "Comparative studies of the amino acid and nucleotide sequences of
RL J. Bacteriol. 164:571-577(1985)."

RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 15652 / PAO1;
RX MEDLINE=20437337; PubMed=10984043;
RA Stryer C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltz L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Lardig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
RT opportunistic pathogen.";
RT Nature 406:959-964(2000).
RN [3]
RP MUTAGENESIS OF GLU-11.
RX MEDLINE=93321167; PubMed=8330261;
RA Macdonald D.L., Pasloske B.L., Paranchych W.;
RT "Mutations in the fifth-position glutamate in Pseudomonas aeruginosa
RT pilin affect the transmethylation of the N-terminal phenylalanine.";
RN Can. J. Microbiol. 39:500-505(1993).

RN [4]
RP STRUCTURE BY NMR OF 132-149.
RX MEDLINE=96110702; PubMed=8845350;
RA Campbell A.P., McInnes C., Hodges R.S., Sykes B.D.;
RT "Comparison of NMR solution structures of the receptor binding
RT domains of Pseudomonas aeruginosa pili strains PAO, KB7, and PAK:
RT implications for receptor binding and synthetic vaccine design.";
RL Biochemistry 34:16255-16268(1995).
CC -1- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
CC NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
CC CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
CC CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.
CC -1- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL: M11323; AAA25954.1;
DR EMBL: AE004866; AAG07913.1;
DR PIR: A25023; A25023.
DR PDB: 1PAN; 29-JAN-96.
DR PDB: 1PAO; 29-JAN-96.
DR InterPro: IPR001082; PiliN.
DR InterPro: IPR001120; Prok_N_methyln.
DR Pfam: PF00114; PiliN; 1.
DR ProDom: PD000666; PiliN; 1.
DR PROSITE: PS00409; PROKAR_NTER_METHYL; 1.
KW Fimbria; Methylation; 3D-structure; Complete proteome.
FT PROPEP 1 6
FT CHAIN 1 149
FT MOD_RES 7 149 FIMBRIAL PROTEIN.
FT DISULFID 134 147 METHYLATION (BY SIMILARITY).
FT MOTAGEN 11 11 BY SIMILARITY.
FT E->A: METHYLATION OF PHE-7 DECREASED AND
FT LOSS OF PILI ASSEMBLY.
SQ SEQUENCE 149 AA; 15512 MW; 98BC8A6F7B022214 CRC64;

Query Match 47.8%; Score 301.5; DB 1; Length 149;
Best Local Similarity 58.1%; Pred. No. 7.4e-21;
Matches 68; Conservative 12; Mismatches 30; Indels 7; Gaps 4;

QY 8 ARSEGASALASVNPDKTYEALSRGWSYKSGTGDATKKEVPLGVADANKLGTI 64
DB 35 ARSEGASALASVNPDKTYEALSRGWSYKSGTGDATKKEVPLGVADANKLGTI 92
QY 65 ALKPPADGTADITLFTWGMGAGPRNKGKIIITLRTADGLMKCTSDDEQFIPKGC 121
DB 93 AVAIEDS-GAGDITFTFGTSSPRNATKVTILNRT-ADGWACKSTODPMFTPKGC 147


```

RESULT 3
FMCD_PSEAE
ID FMCD_PSEAE STANDARD; PRT; 150 AA.
AC P17837;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE FIMBRIAL PROTEIN PRECURSOR (PILIN) (STRAIN CD).
GN PILA OR FIMA.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
ON NCBI_TaxID=287;
RX MEDLINE-88138467; PubMed-2893774;
RA Pasloske B.L., Joffe A.M., Sun Q., Volpel K., Paranchych W.,
RA Eftekhar F., Speert D.P.;
RT "Serial isolates of Pseudomonas aeruginosa from a cystic fibrosis
RT patient have identical pilin sequences.";
RL Infect. Immun. 56:665-672(1988).
CC -1 SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
CC NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
CC CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
CC CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.
CC -1 SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY. ALMOST IDENTICAL
CC TO PA103 PILIN.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
DR EMBL; M24281; AAA25945.1; ALT_INIT.
DR PIR; A43504; A43504.
DR HSSP; P02973; INTL.
DR InterPro; IPR001082; Pilin.
DR InterPro; IPR001120; Prok_N_methyltn.
DR Pfam; PF00114; Pilin; 1.
DR ProDom; PD000666; Pilin; 1.
DR PROSITE; PS00409; PROKAR_NTER_METHYL; 1.
KW Fimbria; Methylation.
FT PROPEP 1 6 FIMBRIAL PROTEIN.
FT CHAIN 7 150 METHYLATION (BY SIMILARITY).
FT MOD_RES 7 7 BY SIMILARITY.
FT DISULFD 134 147
SQ SEQUENCE 150 AA; 15743 MW; E14316996F270F3C CRC64;

Query Match 46.7%; Score 294.5; DB 1; Length 150;
Best Local Similarity 55.9%; Pred. No. 3.2e-20;
Matches 66; Conservative 16; Mismatches 31; Indels 5; Gaps 4;

OY 8 ARSEGASALASVNPDKTVEALSRSQWS-VKSGTGEDATKKEVPLGVAADANKLIGTAL 66
DB 35 ARSEGASALATINPLKTYVESLSRNGISGLITGTASTADTYVIGIDEKANKLGTAV 94

OY 67 K-PDPADGTADITLFTMGAGPKKKKGIITLRTPADGLMKCTSDODEPIPKGCSR 123
DB 95 TIKDGDGT--VKTFEATGSSPKNAGKEITLNR-AGEVWCTSTOEEMFIKGCNK 149

RESULT 4
FMP3_PSEAE STANDARD; PRT; 150 AA.
AC FMP3_PSEAE
ID FMP3_PSEAE
DT 01-AUG-1988 (Rel. 08, Created)

```

```

DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE FIMBRIAL PROTEIN PRECURSOR (PILIN) (STRAIN PA103).
GN PILA OR FIMA.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
ON NCBI_TaxID=287;
RX MEDLINE-87057209; PubMed-2430961;
RA Johnson K., Parker M.L., Loir S.;
RT "Nucleotide sequence and transcriptional initiation site of two
RT Pseudomonas aeruginosa pilin genes.";
RL J. Biol. Chem. 261:15703-15708(1986).
CC -1 SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
CC NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
CC CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
CC CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.
CC -1 SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY. ALMOST IDENTICAL
CC TO CD1 PILIN.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
DR EMBL; M14850; AAA25953.1; -.
DR PIR; B24603; B24603.
DR HSSP; P02973; INTL.
DR InterPro; IPR001082; Pilin.
DR InterPro; IPR001120; Prok_N_methyltn.
DR Pfam; PF00114; Pilin; 1.
DR ProDom; PD000666; Pilin; 1.
DR PROSITE; PS00409; PROKAR_NTER_METHYL; 1.
KW Fimbria; Methylation.
FT PROPEP 1 6 FIMBRIAL PROTEIN.
FT CHAIN 7 150 METHYLATION (BY SIMILARITY).
FT MOD_RES 7 7 BY SIMILARITY.
FT DISULFD 134 147
SQ SEQUENCE 150 AA; 15799 MW; DBDAE8453D4DC85 CRC64;

Query Match 45.2%; Score 285.5; DB 1; Length 150;
Best Local Similarity 55.6%; Pred. No. 2.1e-19;
Matches 65; Conservative 15; Mismatches 32; Indels 5; Gaps 4;

OY 8 ARSEGASALASVNPDKTVEALSRSQWS-VKSGTGEDATKKEVPLGVAADANKLIGTAL 66
DB 35 ARSEGASALATINPLKTYVESLSRNGISGLITGTASTADTYVIGIDEKANKLGTAV 94

OY 67 K-PDPADGTADITLFTMGAGPKKKKGIITLRTPADGLMKCTSDODEPIPKGCSR 122
DB 95 TIKDGDGT--IKFNFATGSSPKNAGREITLNR-AGEVWCTSTOEEMFIKGCNK 148

RESULT 5
FMAH_BACNO STANDARD; PRT; 156 AA.
AC FMAH_BACNO
ID FMAH_BACNO
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 01-NOV-1991 (Rel. 20, Last annotation update)
DE FIMBRIAL PROTEIN PRECURSOR (PILIN) (SEROGROUP H1) (265 ANTIGEN) (TWO
DE SUBUNITS PILIN).
GN FIMA.
OS Bacteroides nodosus (Dichelobacter nodosus).
OC Bacteria; Proteobacteria; gamma subdivision; Cardiobacteriaceae;
OC Dichelobacter.

```

```

FMPL_PSEAE
ID FMPL_PSEPE STANDARD: PRT; 157 AA.
AC P17838;
DT 01-AUG-1990 (Rel. 15, Created)
DI 01-AUG-1990 (Rel. 15, Last sequence update)
DE 01-JUN-1994 (Rel. 29, Last annotation update)
DE FIMBRIAL PROTEIN PRECURSOR (PILIN) (STRAIN PI).
GN PILA OR FIMA.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=PI.
RX MEDLINE=88296689; PubMed=2841299.
RA Pasloske B.L., Sastiy P.A., Finlay B.B., Paranchych W.;
RT "Two unusual pilin sequences from different isolates of Pseudomonas
aeruginosa.";
RL J. Bacteriol. 170:378-3741(1988).
-1- SUBUNIT: THE PIL ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
CONFIGURATION OF FIVE SUBUNTS PER TURN IN THE ASSEMBLED PILUS.
-1- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sdb.ch/announce/
CC or send an email to license@isb-sdb.ch).
CC
CC EMBL: M21651; AAC63062.1; -
CC
CC PIR: A31105; A31105.
CC
CC HSSP: P02974; 1A72.
CC
CC InterPro: IPR001082; Pilin.
CC InterPro: IPR001120; Prok_N_methyltn.
CC Pfam: PF00114; pilin; 1.
CC Prodom: PD000666; pilin; 1.
CC PROSITE: PS00409; PROKAR_NTER_METHYL; 1.
CC
CC KW fimbria; methylation.
CC
CC PROPEP 1 157
CC CHAIN 7 FIMBRIAL PROTEIN.
CC MOD_RES 8 8 METHYLATION (BY SIMILARITY).
CC DISULFID 136 149 BY SIMILARITY.
CC
CC SO SEQUENCE 157 AA; 16175 MW; 234E37B1D5C1EA49 CRC64;
-----
Query Match 17.6%; Score 111; DB 1; Length 157;
Best Local Similarity 27.7%; Pred. No. 0.0018;
Matches 33; Conservative 17; Mismatches 59; Indels 10; Gaps 3;
OY 8 ARSEASALASVNPATKTYVEALSLGWSVSGTGTGEDATKEVPLG--VAADANKLCTIA 65
DI ::::: ::::: ::::: :::::
DB 36 ARAQLSERMTLASLGKTVSDIFSDGSCPANTATAGIEKDTINGRYAKVYTGCTAA 95
OY 66 LKPDADGTADITTLFTMGAGAPRNKRIITLFTAADG--LKCTSDDEQPIPGC 121
DI ::::: ::::: ::::: :::::
DB 96 ----ASGGCTIVATMKASDVATPLRKGTLLTLTGNDKSGSYTACTSNADNKILPTFC 149
-----
RESULT 7
FMWC_PSEPU STANDARD; PRT; 136 AA.
ID FMWC_PSEPU
AC P36643;
DT 01-JUN-1994 (Rel. 29, Created)
DI 01-JUN-1994 (Rel. 29, Last sequence update)
DE 01-OCT-1994 (Rel. 30, Last annotation update)
DE FIMBRIAL PROTEIN PRECURSOR (PILIN).
GN PILA.
OS Pseudomonas putida.

```

OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas
 OX NCBI_TaxID=303;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MCS358;
 RX MEDLINE=94131942; PubMed=7905475;
 RA de Groot A., Heijnen I., de Cock H., Filloux A., Tommassen J.;
 RT "Characterization of type IV pilus genes in plant growth-promoting
 Pseudomonas putida WCS358.";
 RL J. Bacteriol. 176:642-650(1994).
 CC -1- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X74276; CAA52332.1; -;
 DR PIR: S35951; S35951.
 DR HSSP: P02974; IAY2.
 DR InterPro: IPR001082; Piliin.
 DR InterPro: IPR001120; Prok_N_methyltn.
 DR Pfam: PF00114; Piliin; 1.
 DR ProDom: PD000666; Piliin; 1.
 DR PROSITE: PS00409; PROKAR_NTER_METHYL; 1.
 KW Fimbria; Methylation.
 FT PROPEP 1 6 POTENTIAL.
 FT CHAIN 7 136 FIMBRIAL PROTEIN
 FT MOD_RES 7 7 METHYLATION (BY SIMILARITY).
 FT DISULFID 120 133 BY SIMILARITY.
 SQ SEQUENCE 136 AA; 13632 MW; B3C3BB3333E5D5CF CRC64;
 Query Match 17.2%; Score 108.5; DB 1; Length 136;
 Best Local Similarity 28.7%; Pred. No. 0.0026;
 Matches 35; Conservative 16; Mismatches 40; Indels 31; Gaps 5;
 OY 8 ARSBSASALASVNPDKTVEEALSRGMSVSGTGTEDEATKKEVPLGVAADANKLG----- 62
 Db 35 SRTAAAGLEISALKTRMDRLNMG-----KDV-----ADGAGAGGOGPAT 75
 OY 63 ---TALKPDPADGTADITLFTTWGAGPKNKRIITLRTADGLMKCTSDODEQETPK 119
 Db 76 AHCAITASGNMAAGTSIVCTLV--DAPATVVGKALTLTTSATG--MCTTINIEDLAPS 131
 OY 120 GC 121
 Db 132 GC 133
 RESULT 8
 FMO_MORBO STANDARD; PRT; 157 AA.
 AC P07640;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE FIMBRIAL PROTEIN Q PRECURSOR (BETA PILIN) (Q PILIN).
 GN TPEQ.
 OS Moraxella bovis.
 OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae; Moraxella.
 OX NCBI_TaxID=476;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EPP63;
 RX MEDLINE=85234350; PubMed=2861194;
 RA Maris C.F., Schoolnik G., Koomey J.M., Hardy J., Rothbard J.,
 RA Falkow S.;
 RT "Cloning and sequencing of a Moraxella bovis pilin gene.";
 RT

RL J. Bacteriol. 163:132-139(1985).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EPP63;
 RX MEDLINE=90094235; PubMed=2403542;
 RA Fults K.A., Maris C.F., Stevens S.P., Green M.R.;
 RT "Sequence analysis of the inversion region containing the pilin genes
 of Moraxella bovis.";
 RL J. Bacteriol. 172:310-316(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91286182; PubMed=2061282;
 RA Rosa F.M., Maris C.F.;
 RT "Interesting sequence differences between the pilin gene inversion
 regions of Moraxella lacunata ATCC 17956 and Moraxella bovis Epp63.";
 RL J. Bacteriol. 173:4000-4006(1991).
 RN [4]
 RP SEQUENCE OF 7-157.
 RX MEDLINE=89010522; PubMed=2902184;
 RA Ruehl W.W., Maris C.F., Fernandez R., Falkow S., Schoolnik G.K.;
 RT "Purification, characterization, and pathogenicity of Moraxella bovis
 pilin.";
 RL J. Exp. Med. 168:983-1002(1988).
 CC -1- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
 CC NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
 CC CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
 CC CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.
 CC -1- MISCELLANEOUS: MORAXELLA BOVIS CAN EXPRESS EITHER A Q OR A I
 CC PILIN. THE INVERSION OF 2 KB OF DNA DETERMINES WHICH PILIN IS
 CC EXPRESSED.
 CC -----
 CC -1- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M11435; AAA25304.1; -;
 DR EMBL: M32345; AAA88223.1; -;
 DR PIR: M59712; AAA25308.1; -;
 DR PIR: A24434; A24434.
 DR PIR: J10072; J10072.
 DR InterPro: IPR001082; Piliin.
 DR InterPro: IPR001120; Prok_N_methyltn.
 DR Pfam: PF00114; Piliin; 1.
 DR ProDom: PD000666; Piliin; 1.
 DR PROSITE: PS00409; PROKAR_NTER_METHYL; 1.
 KW Fimbria; Methylation.
 FT PROPEP 1 6 FIMBRIAL PROTEIN Q.
 FT CHAIN 7 157
 FT MOD_RES 7 7 METHYLATION.
 FT DISULFID 136 155 BY SIMILARITY.
 SQ SEQUENCE 157 AA; 16006 MW; A923CD8A26C93C9 CRC64;
 Query Match 16.2%; Score 102.5; DB 1; Length 157;
 Best Local Similarity 28.2%; Pred. No. 0.011;
 Matches 35; Conservative 25; Mismatches 51; Indels 13; Gaps 6;
 OY 8 ARSBSASALASVNPDKTVEEALSRGMSVSGTGTEDEATKKEVPL---GVAADANKLGTI 64
 Db 35 SKSQTRVYGEIAAGKTAVDALFEKTPKLGKAAAND--TERDIGITTTGTAARSMLSSV 93
 OY 65 ALKPDPAAGTADITLFTTWGAGPKNK-RGKIITLRTADGLMKCTSDQD-----EQFI 117
 Db 94 NI-GGGAATGATGATLEATLGNANKNDIGAVITQSRD-AEGWVCTINGSAAPGKSKFV 151
 OY 118 PKGC 121
 Db 152 PTGC 155

RESULT 9
FM12_PSEAE STANDARD: PRT: 154 AA.
AC P18774;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE FIMBRIAL PROTEIN PRECURSOR (PILIN) (STRAIN 1244).
GN PILA OR FIMA.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89281493; PubMed=2499765;
RA Castic P.A., Siderberry H.F., Sadoff J.C.;
RT "Cloning and sequencing of the Pseudomonas aeruginosa 1244 pilin
structural gene."
RL Mol. Gen. Genet. 216:75-80(1989).
CC -1- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.
CC -1- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X83916; CAA58768.1; -
DR PIR: S04440; S04440.
DR HSSP: P02974; IAY2.
DR InterPro: IPR001082; Pilin.
DR InterPro: IPR001120; Prok_N_methyltn.
DR Pfam: PF00114; Pilin; 1.
DR ProDom: PD000666; Pilin; 1.
DR PROSITE: PS00409; PROKAR_NTER_METHYL; 1.
KW Fimbria; Methylation.
FT PROPEP 1 6
FT CHAIN 7 154
FT MOD_RES 7 7 FIMBRIAL PROTEIN.
FT DISULFID 133 151 METHYLATION (BY SIMILARITY).
FT SEQUENCE 154 AA; 16277 MW; 9A6E09E0A6C66AD0 CRC64;

Query Match 15.8%; Score 99.5; DB 1; Length 154;
Best Local Similarity 27.6%; Pred. No. 0.019;
Matches 35; Conservative 22; Mismatches 51; Indels 19; Gaps 7;

OY 8 ARSEASALASVNPDKTVEEALSRGWSVKSCTGTEADTKKEVPLGYAADANKL-----GT 63
DB 35 ARTQYTRAVSEVSAKTKTAESAIIIEGKEIVS-----SATPKDQYDYGTFESTILLDSGK 89
OY 64 IALK-PDPAAGTADITLFTMG-GAGPRNKGIITLRTADAGLMKCTSO-----DEOF 116
DB 90 SQIQVTDNKGDT--VEIVATLGRSGSAIKGAVITVSR-KNDGYWNCIKTKTPAMKPNY 146
OY 117 IPKCSR 123
DB 147 APANCPK 153
RESULT 10
FMK1_PSEAE STANDARD: PRT: 154 AA.
AC P17836;

DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE FIMBRIAL PROTEIN PRECURSOR (PILIN) (STRAIN K122-4).
GN PILA OR FIMA.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K122-4;
RX MEDLINE=88298689; PubMed=2841299;
RA Pasloske B.L., Sastly P.A., Finlay B.B., Paranchych W.;
RT "Two unusual pilin sequences from different isolates of Pseudomonas
aeruginosa."
RL J. Bacteriol. 170:3738-3741(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-9D2;
RX MEDLINE=94131566; PubMed=7507890;
RA Castic P.A., Deal C.D.;
RT "Differentiation of Pseudomonas aeruginosa pili based on sequence and
B-cell epitope analyses."
RL Infect. Immun. 62:371-376(1994).
CC -1- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.
CC -1- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M21652; AAC63060.1; -
DR PIR: B31105; B31105.
DR HSSP: P02974; IAY2.
DR InterPro: IPR001082; Pilin.
DR InterPro: IPR001120; Prok_N_methyltn.
DR Pfam: PF00114; Pilin; 1.
DR ProDom: PD000666; Pilin; 1.
DR PROSITE: PS00409; PROKAR_NTER_METHYL; 1.
KW Fimbria; Methylation.
FT PROPEP 1 6
FT CHAIN 7 154
FT MOD_RES 7 7 FIMBRIAL PROTEIN.
FT DISULFID 133 151 METHYLATION (BY SIMILARITY).
FT SEQUENCE 154 AA; 16278 MW; 807409FAACC66AD0 CRC64;

Query Match 15.8%; Score 99.5; DB 1; Length 154;
Best Local Similarity 27.6%; Pred. No. 0.019;
Matches 35; Conservative 22; Mismatches 51; Indels 19; Gaps 7;

OY 8 ARSEASALASVNPDKTVEEALSRGWSVKSCTGTEADTKKEVPLGYAADANKL-----GT 63
DB 35 ARTQYTRAVSEVSAKTKTAESAIIIEGKEIVS-----SATPKDQYDYGTFESTILLDSGK 89
OY 64 IALK-PDPAAGTADITLFTMG-GAGPRNKGIITLRTADAGLMKCTSO-----DEOF 116
DB 90 SQIQVTDNKGDT--VEIVATLGRSGSAIKGAVITVSR-KNDGYWNCIKTKTPAMKPNY 146
OY 117 IPKCSR 123
DB 147 APANCPK 153

```

RESULT 11
FMZH_BACNO STANDARD: PRT: 159 AA.
ID FMZH_BACNO STANDARD: PRT: 159 AA.
AC P17417;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE POSSIBLE MINOR FIMBRIAL PROTEIN PRECURSOR (PILIN) (SEROGROUP H1).
GN FIMZ.
OS Bacteroides nodosus (Dichelobacter nodosus).
OC Bacteria; Proteobacteria; gamma subdivision; Cardiobacteriaceae;
OC Dichelobacter.
OX NCBI_TaxID=870;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SEROGROUP H1 ISOLATE VCS1215;
RX MEDLINE=91260439; PubMed=1675418;
RA Hobbs M., Dalrymple B.P., Cox P.T., Livingstone S.P., Delaney S.F.,
RA Mattick J.S.;
RT "Organization of the fimbrial gene region of Bacteroides nodosus:
RT class I and class II strains."
RL Mol. Microbiol. 5:543-560(1991).
CC -1- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
CC NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
CC CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
CC CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.
CC -1- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC
DR EMBL: X52390; CAA36622.1;
DR PIR: S15251; YOBZHZ.
DR HSSP: P02974; IAY2.
DR InterPro: IPR001082; PiliN.
DR InterPro: IPR001120; Prok_N_methyltn.
DR Pfam: PF00114; PiliN; 1.
DR ProDom: PD000666; PiliN; 1.
DR PROSITE: PS00409; PROKAR_NTER_METHYL; 1.
KM Fimbria; Methylation.
FT PROPEP 1 159 POSSIBLE MINOR FIMBRIAL PROTEIN.
FT CHAIN 7 7 METHYLATION (BY SIMILARITY).
FT MOD_RES 56 71 BY SIMILARITY.
FT DISULFD 140 153 BY SIMILARITY.
FT DISULFD 140 153 BY SIMILARITY.
SQ SEQUENCE 159 AA; 17188 MW; 7D928B7E0A8BDC5 CRC64;

Query Match 15.6%; Score 98.5; DB 1; Length 159;
Best Local Similarity 24.8%; Pred. No. 0.025;
Matches 30; Conservative 20; Mismatches 60; Indels 11; Gaps 3;
OY 9 RSEGSALASVPLKTTVEALSRSKVSXSGTGEDATKEVPLGVADANKLGTALK- 67
DB 36 RSOQVRLMEAGELRLAVQCLNDG-TTRKIGNGNECCDPRASGNISGASQNPETVIA 94
OY 68 -----PDPADGTADITLFTFTMGAGPKNKGIITLFTTADGIMKCTSDDEQIFPG 120
DB 95 NTGVVQFPNPLTEETALTATFNNSASIIHGKLLI--WQROKSGSWYCHSNAEKFLPSG 152
OY 121 C 121
DB 153 C 153

RESULT 12
FMZD_BACNO STANDARD: PRT: 159 AA.
ID FMZD_BACNO STANDARD: PRT: 159 AA.

```

```

AC P17416;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE POSSIBLE MINOR FIMBRIAL PROTEIN PRECURSOR (PILIN) (SEROGROUP D).
GN FIMZ.
OS Bacteroides nodosus (Dichelobacter nodosus).
OC Bacteria; Proteobacteria; gamma subdivision; Cardiobacteriaceae;
OC Dichelobacter.
OX NCBI_TaxID=870;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SEROGROUP D ISOLATE VCS1172;
RX MEDLINE=91260439; PubMed=1675418;
RA Hobbs M., Dalrymple B.P., Cox P.T., Livingstone S.P., Delaney S.F.,
RA Mattick J.S.;
RT "Organization of the fimbrial gene region of Bacteroides nodosus:
RT class I and class II strains."
RL Mol. Microbiol. 5:543-560(1991).
CC -1- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
CC NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
CC CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
CC CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.
CC -1- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC
DR EMBL: X52389; -; NOT_ANNOTATED_CDS.
DR PIR: S15249; YOBZDZ.
DR HSSP: P02974; IAY2.
DR InterPro: IPR001082; PiliN.
DR InterPro: IPR001120; Prok_N_methyltn.
DR Pfam: PF00114; PiliN; 1.
DR ProDom: PD000666; PiliN; 1.
DR PROSITE: PS00409; PROKAR_NTER_METHYL; 1.
KM Fimbria; Methylation.
FT PROPEP 1 159 POSSIBLE MINOR FIMBRIAL PROTEIN.
FT CHAIN 7 7 METHYLATION (BY SIMILARITY).
FT MOD_RES 56 71 BY SIMILARITY.
FT DISULFD 140 153 BY SIMILARITY.
FT DISULFD 140 153 BY SIMILARITY.
SQ SEQUENCE 159 AA; 17102 MW; E538B0DC52B88C82 CRC64;

Query Match 14.8%; Score 93.5; DB 1; Length 159;
Best Local Similarity 24.0%; Pred. No. 0.071;
Matches 29; Conservative 20; Mismatches 61; Indels 11; Gaps 3;
OY 9 RSEGSALASVPLKTTVEALSRSKVSXSGTGEDATKEVPLGVADANKLGTALK- 67
DB 36 RSOQVRLMEAGELRLAVQCLNDG-TTVGNGNECCDPRASGNISGASQNPETVIA 94
OY 68 -----PDPADGTADITLFTFTMGAGPKNKGIITLFTTADGIMKCTSDDEQIFPG 120
DB 95 NTGVVQFPNPLTEETALTATFNNSASIIHGKLLI--WQROKSGSWYCHSNAEKFLPSG 152
OY 121 C 121
DB 153 C 153

RESULT 13
ECPC_EIKCO STANDARD: PRT: 153 AA.
ID ECPC_EIKCO STANDARD: PRT: 153 AA.
AC 007564;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)

```

DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE FIMBRIAL PROTEIN ECPC PRECURSOR (PILIN).
 GN ECPC.
 OS Eikenella corrodens.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Eikenella.
 OX NCBI_TaxID=539;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=31745;
 RX MEDLINE=93339296; PubMed=8478080;
 RA Tonjum T., Weir S., Boyre K., Prognulské-Fox A., Marrs C.F.;
 RT "Sequence divergence in two tandemly located pilin genes of Eikenella corrodens."
 RL Infect. Immun. 61:1909-1916(1993).
 CC -1- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: L12049; AAA03016.1; -.
 DR HSSP: P02974; IAY2.
 DR InterPro: IPR001082; Pilin.
 DR InterPro: IPR001120; Prok_N_methyltn.
 DR Pfam: PF00114; Pilin; 1.
 DR ProDom: PD000666; Pilin; 1.
 DR PROSITE: PS00409; PROKAR_NTER_METHYL; 1.
 KW Fimbrin; Methylation.
 FT PROPEP 1 8 POTENTIAL.
 FT CHAIN 9 153 FIMBRIAL PROTEIN ECPC.
 FT MOD_RES 9 9 METHYLATION (BY SIMILARITY).
 FT DISULFID 130 143 BY SIMILARITY.
 FT SEQUENCE 153 AA; 15695 MW; 03A98B1C8AFAA053 CRC64;

Query Match 14.7%; Score 92.5; DB 1; Length 153;
 Best Local Similarity 27.1%; Pred. No. 0.083;
 Matches 32; Conservative 15; Mismatches 56; Indels 15; Gaps 4;

OY 8 ANSEGASALASVPLKTYEALS-RG-MSVSGSTGTEDEATKKEVPLGVAADANKGTIA 65
 DB 37 ANSOMESEARNLGCGKGVSEYSDSGVWPADNAA-----GTAATVNGKYVNS 85
 OY 66 LKPPADGTADITLFTMGAGPKNKKITTLRTADG--LWKCTSDDEQFIPKGC 121
 DB 86 VVVSAGTNGVITATKSTGVAKGVGKTLALKGTANDGSFSEWSSNDAKYLPSSC 143

RESULT 14

FML_MORBO
 ID FMI_MORBO STANDARD; PRT; 159 AA.
 AC P20657;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE FIMBRIAL PROTEIN I PRECURSOR (ALPHA PILIN) (I PILIN).
 OS Moraxella bovis.
 OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae; Moraxella.
 OX NCBI_TaxID=476;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EP63;
 RX MEDLINE=90094235; PubMed=2403542;
 RA Fuks R.A., Marrs C.F., Stevens S.P., Green M.R.;
 RT "Sequence analysis of the inversion region containing the pilin genes
 RT of Moraxella bovis."
 RL J. Bacteriol. 172:310-316(1990).
 RN [2]
 RP SEQUENCE OF 7-159.

RX MEDLINE=89010522; PubMed=2902184;
 RA Ruelh W.W., Marrs C.F., Fernandez R., Falkow S., Schoolnik G.K.;
 RT "Purification, characterization, and pathogenicity of Moraxella bovis
 RT pilin."
 RL J. Exp. Med. 168:983-1002(1988).
 CC -1- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
 CC NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
 CC CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
 CC CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.
 CC MISCELLANEOUS: MORAXELLA BOVIS CAN EXPRESS EITHER A Q OR A I
 CC PILIN, THE INVERSION OF 2 KB OF DNA DETERMINES WHICH PILIN IS
 CC EXPRESSED.
 CC -1- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: M32345; -; NOT_ANNOTATED_CDS.
 DR PIR: JL0071; JL0071.
 DR HSSP: P02974; IAY2.
 DR InterPro: IPR001082; Pilin.
 DR InterPro: IPR001120; Prok_N_methyltn.
 DR Pfam: PF00114; Pilin; 1.
 DR ProDom: PD000666; Pilin; 1.
 DR PROSITE: PS00409; PROKAR_NTER_METHYL; 1.
 KW Fimbrin; Methylation.
 FT PROPEP 1 6
 FT CHAIN 7 159 FIMBRIAL PROTEIN I.
 FT MOD_RES 7 7 METHYLATION.
 FT CONFLICT 159 159 K -> KSK (IN REF. 2).
 FT SEQUENCE 159 AA; 16723 MW; 9130E2289CF679E CRC64;

Query Match 14.4%; Score 91; DB 1; Length 159;
 Best Local Similarity 24.1%; Pred. No. 0.12;
 Matches 27; Conservative 22; Mismatches 45; Indels 18; Gaps 4;

OY 23 KTTVEEALSRGMSVSKSTGTEDEATKKEVPLGVAAD-----ANKIGTALKRPPADGTA 75
 DB 50 KTAVDALAEQ---KTPVLSSESSSTKENIGLSTSTKPSNLMASVELIGPADNGAG 106
 OY 76 DITLFTMGAGPKNKKITTLRTADGIMKCTSD-----QDEQFIPKGC 121
 DB 107 --TISATLGNKANKNDIAKTVITQERTDGVWICKIDSGAAKYKEKFNPTGC 156

RESULT 15

FMAJ_BACNO
 ID FMAJ_BACNO STANDARD; PRT; 160 AA.
 AC P19528;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last annotation update)
 DE FIMBRIAL PROTEIN I PRECURSOR (PILIN) (SEROGROUP H) (351 ANTIGEN).
 GN FIMA.
 OS Bacteroides nodosus (Dichelobacter nodosus).
 OC Bacteria; Proteobacteria; gamma subdivision; Cardiobacteriaceae;
 OC Dichelobacter.
 OX NCBI_TaxID=870;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SEROGROUP H ISOLATE 351;
 RX MEDLINE=90155189; PubMed=2621448;
 RA Hoyne P.A., Eillemann T.C., McKern N.M., Stewart D.J.;
 RT "Sequence of pilin from Bacteroides nodosus 351 (Serogroup H) and
 RT implications for serogroup classification."
 RL J. Gen. Microbiol. 135:1113-1122(1989).
 CC -1- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4

```

CC      NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH. THEY
CC      CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
CC      CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.
CC      -1- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
CC      -----
CC      THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; M26980; AAA23336.1; -.
DR      PIR; A37167; A37167.
DR      HSSP; Q53391; 1KB8.
DR      InterPro: IPR001082; PiliN.
DR      InterPro: IPR001120; Prok_N_methyltn.
DR      Pfam; PF00114; PiliN; 1.
DR      ProDom; PD000666; PiliN; 1.
DR      ProSite; PS00409; PROKAR_NTER_METHYL; 1.
KW      Fimbria; Methylation.
FT      PROPEP 1
FT      CHAIN 8 160 FIMBRIAL PROTEIN.
FT      MOD_RES 8 8 METHYLATION (BY SIMILARITY).
SQ      SEQUENCE 160 AA; 17169 MW; 3160DAFAE8/ABAA CRC64;

Query Match 14.1%; Score 89; DB 1; Length 160;
Best Local Similarity 25.4%; Pred. No. 0.18;
Matches 33; Conservative 17; Mismatches 54; Indels 26; Gaps 5;

QY      8 ARSEGASALASVNPDKTTVEALS-----GWSVK-----SGTGTEDAATKKEVP 51
DB      36 ARSQVSRVSESGQMRFAIEFTCLDGKKADCEFIGWTKSNLIGASGSPSSNDSTADHPG 95

QY      52 LGVAADANKLGTALKPPACGTADITLFTMGANGPKNKRIITLRTAADGLKCTSD 111
DB      96 QGGIVIDYKL-----EADATNAITATFGONAAATLH-GKALKWTRD-PRATWSCSTD 145

QY      112 QDEOFIPKGC 121
DB      146 VELKFRPRGC 155

```

Search completed: February 8, 2002, 15:34:21
 Job time: 546 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 8, 2002, 15:24:35 ; Search time 67.44 Seconds

(without alignments)
266.778 Million cell updates/sec

Title: US-09-865-159-4

Sequence: 1 ALDEGTFEAFSEGASALASVN.....GLMKCTSDODEQFIRKCSR 123

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP_PROTOCTIST:*
12: SP_VIRUS:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	299.5	47.5	150	2	Q59795 pseudomonas
2	130	20.6	139	2	Q9ZEL3 pseudomonas
3	129.5	20.6	140	2	Q9F671 pseudomonas
4	126.5	20.0	136	2	Q56799 xanthomonas
5	117	18.5	147	2	Q30583 acinetobact
6	115.5	18.3	145	2	Q52613 xanthomonas
7	111.5	17.7	145	2	Q9APK5 xanthomonas
8	110.5	17.5	130	2	Q9S4E2 bacteroides
9	109.5	17.4	153	2	Q9X4G7 vibrio chol
10	109.5	17.4	167	2	Q9KPE5 vibrio chol
11	109	17.3	148	2	Q9PAH6 xyloella fas
12	105.5	16.7	154	2	Q59794 pseudomonas
13	104	16.5	159	2	Q60163 moraxella b
14	99	15.7	148	2	Q9PAH9 xyloella fas
15	95.5	15.1	130	2	Q9APJ4 xanthomonas
16	94	14.9	134	2	Q9S4E1 bacteroides
17	93	14.7	157	2	Q59503 moraxella b
18	92.5	14.7	116	2	Q9APJ3 xanthomonas
19	89	14.1	159	2	Q59505 moraxella b

20	89	14.1	350	2	Q9CFM9 lactococcus
21	87	13.8	218	2	Q69813 streptomyces
22	86.5	13.7	1128	1	Q51999 halobacteri
23	86	13.6	131	2	Q9AP36 bacteroides
24	86	13.6	157	2	Q59336 dichelobact
25	85.5	13.5	156	2	Q59507 moraxella b
26	83	13.2	158	2	Q59508 moraxella b
27	81.5	12.9	163	2	Q9L9W0 neisseria c
28	81	12.8	515	11	Q9QY61 mus musculu
29	81	12.8	713	2	Q9FC87 streptococ
30	81	12.8	1587	10	Q9LQES arbidopsi
31	80	12.7	385	2	Q9X7Z3 streptococ
32	79.5	12.6	158	2	Q54650 bacteroides
33	79.5	12.6	160	2	Q59504 moraxella b
34	79.5	12.6	539	2	Q9RK08 streptomyces
35	79.5	12.6	856	3	Q74170 aspergillus
36	78.5	12.4	131	2	Q9S4E3 bacteroides
37	78.5	12.4	135	2	Q56800 xanthomonas
38	78	12.4	360	5	Q9NE18 leishmania
39	77.5	12.3	158	2	Q59501 moraxella b
40	77.5	12.3	284	3	Q9HFP8 aspergillus
41	77.5	12.3	552	4	Q9NTZ8 homo sapien
42	77	12.2	515	1	Q9Y9T6 aeropyrum p
43	76.5	12.1	94	2	Q9S1P0 streptomyces
44	76.5	12.1	350	2	Q99ZM4 streptococ
45	76.5	12.1	474	5	Q9XXQ2 caenorhabdi

ALIGNMENTS

RESULT	1	PRELIMINARY;	PRT;	150 AA.
Q59795	Q59795	Q59795	Q59795	Q59795
ID	Q59795	Q59795	Q59795	Q59795
AC	Q59795	Q59795	Q59795	Q59795
DT	01-JUN-1998 (TREMBLrel. 06, Created)	01-JUN-1998 (TREMBLrel. 06, Last sequence update)	01-JUN-1998 (TREMBLrel. 17, Last annotation update)	01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE	FIBRILLAL PROTEIN PRECURSOR (PILIN) (STRAIN T2A).	PILA OR FIMA.	Pseudomonas aeruginosa.	Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
GN	PILA OR FIMA.	Pseudomonas aeruginosa.	Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;	Pseudomonas
OC	Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;	Pseudomonas	Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;	Pseudomonas
OX	NCBI_TaxID=287;	NCBI_TaxID=287;	NCBI_TaxID=287;	NCBI_TaxID=287;
RN	(1)	(1)	(1)	(1)
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	STRAIN-T2A;	STRAIN-T2A;	STRAIN-T2A;	STRAIN-T2A;
RX	MEDLINE=94131566; PubMed=7507890;	MEDLINE=94131566; PubMed=7507890;	MEDLINE=94131566; PubMed=7507890;	MEDLINE=94131566; PubMed=7507890;
RA	Castric P.A., Deal C.D.;	Castric P.A., Deal C.D.;	Castric P.A., Deal C.D.;	Castric P.A., Deal C.D.;
RT	"Differentiation of Pseudomonas aeruginosa pill based on sequence and	"Differentiation of Pseudomonas aeruginosa pill based on sequence and	"Differentiation of Pseudomonas aeruginosa pill based on sequence and	"Differentiation of Pseudomonas aeruginosa pill based on sequence and
RL	B-cell epitope analyses.";	B-cell epitope analyses.";	B-cell epitope analyses.";	B-cell epitope analyses.";
RR	Infect. Immun. 62:371-376(1994).	Infect. Immun. 62:371-376(1994).	Infect. Immun. 62:371-376(1994).	Infect. Immun. 62:371-376(1994).
CC	-1 SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4	-1 SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4	-1 SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4	-1 SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
CC	NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY	NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY	NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY	NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
CC	CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL	CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL	CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL	CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
CC	CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.	CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.	CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.	CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.
CC	-1 SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.	-1 SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.	-1 SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.	-1 SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
DR	EMBL: S68102; AAC60462.1;	EMBL: S68102; AAC60462.1;	EMBL: S68102; AAC60462.1;	EMBL: S68102; AAC60462.1;
DR	HSSP: P02973; INTL.	HSSP: P02973; INTL.	HSSP: P02973; INTL.	HSSP: P02973; INTL.
DR	InterPro: IPR001082; Pili.	InterPro: IPR001082; Pili.	InterPro: IPR001082; Pili.	InterPro: IPR001082; Pili.
DR	InterPro: IPR001120; Pili.	InterPro: IPR001120; Pili.	InterPro: IPR001120; Pili.	InterPro: IPR001120; Pili.
DR	Pfam: PF00114; Pili; 1.	Pfam: PF00114; Pili; 1.	Pfam: PF00114; Pili; 1.	Pfam: PF00114; Pili; 1.
DR	ProDom: PD000666; Pili; 1.	ProDom: PD000666; Pili; 1.	ProDom: PD000666; Pili; 1.	ProDom: PD000666; Pili; 1.
DR	ProSite: PS00409; PROKAR_NTER_METHYL. 1.	ProSite: PS00409; PROKAR_NTER_METHYL. 1.	ProSite: PS00409; PROKAR_NTER_METHYL. 1.	ProSite: PS00409; PROKAR_NTER_METHYL. 1.
KW	Fimbriae; Methylation.	Fimbriae; Methylation.	Fimbriae; Methylation.	Fimbriae; Methylation.
FT	PROPEP 1	PROPEP 1	PROPEP 1	PROPEP 1
FT	CHAIN 7	CHAIN 7	CHAIN 7	CHAIN 7
FT	DISULFD 134	DISULFD 134	DISULFD 134	DISULFD 134
FT	MOD_RES 7	MOD_RES 7	MOD_RES 7	MOD_RES 7
SO	SEQUENCE 150 AA; 15356 MW; A/F21CD92AF3DCFL CRC64;	SEQUENCE 150 AA; 15356 MW; A/F21CD92AF3DCFL CRC64;	SEQUENCE 150 AA; 15356 MW; A/F21CD92AF3DCFL CRC64;	SEQUENCE 150 AA; 15356 MW; A/F21CD92AF3DCFL CRC64;

Query Match

47.5%; Score 299.5; DB 2; Length 150;

Best Local Similarity 58.3%; Pred. No. 5.7e-20;
Matches 67; Conservative 14; Mismatches 31; Indels 3; Gaps 3;

QY 8 ARSEASALASVNPDKTYEALSRGWSVKS-GTGEDATKKEVPLGVAADANKLGTAL 66
DB 35 ARSEASALATINPLKTYEESLSRGISGENIKISQASTADTYGVDAANLGTITAV 94
QY 67 KPDADGTADITLFTMGAGPKNKGIITLRTAADLMKCTSDODEQFIPKGC 121
DB 95 TIG-NGAGCTYFTTAAGNSPKNSGALITLRTDA-GSWACTSTODEMFIKGC 147

RESULT 2

Q9ZEL3 PRELIMINARY; PRT: 139 AA.
AC Q9ZEL3:
DT 01-MAY-1999 (TREMblrel. 10, Created)
DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE TYPE IV PILIN SUBUNIT.
GN PILA OR PILAI.
OS Pseudomonas stutzeri (Pseudomonas perfectmarina).
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
CC Pseudomonas.
OX NCBI_Taxid=316;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-JM300;
RA Graupner S., Wackernagel W.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RP SEQUENCE FROM N.A.
RC STRAIN-JM300;
RA Graupner S., Wackernagel W.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -1 SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS (BY
SIMILARITY).
CC -1 SIMILARITY: BELONGS TO THE FIMBRIAL PROTEIN (N-ME-PHE)PILIN
FAMILY.
DR EMBL: AJ133364; CA10652.1;
DR EMBL: AJ249743; CAB60734.1;
DR InterPro: IPR002416; Bac_GSPH.
DR InterPro: IPR001082; Pilin.
DR InterPro: IPR001120; Prok_N_methyltn.
DR Pfam: PF00114; pilin; 1.
DR PRINTS: PR00885; BCTERIALGSPH.
DR PRODOM: PD000666; pilin; 1.
DR PROSITE: PS00409; PROKAR_NTER_METHYL; 1.
KW Fimbria; Methylation.
FT MOD_RES 9
SEQUENCE 139 AA; 14558 MW; C3C0DCEFOA9EA770 CRC64;

Query Match 20.6%; Score 130; DB 2; Length 139;
Best Local Similarity 36.4%; Pred. No. 0.00014;
Matches 44; Conservative 10; Mismatches 41; Indels 26; Gaps 6;

QY 9 RSEGSALASVNPDKTYEALSRG-----WSVKS-G-TGTEADATK-K-EVPLGVAADANKL 61
DB 38 RSNMAAALAEITPGKIGFEQAINEGKTPSLSTDEGYIGITDSYCDVLDLTRAADG-- 95
QY 62 GTIALKPDADGTADITLFTMGAGPKNKGIITLRTAADLMKCTSDODEQFIPKGC 121
DB 96 -----ICTAGKNAG-KFDGKTITLNR-T-ADGWSGASTLDKAYKPKGC 138
QY 122 S 122
DB 139 S 139

RESULT 3

Q9F671 PRELIMINARY; PRT: 140 AA.
AC Q9F671:
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE PILIN MAJOR SUBUNIT.
GN PILA.
OS Pseudomonas fluorescens.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
CC Pseudomonas.
OX NCBI_Taxid=294;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WCS365;
RA Camacho Carvajal M.M., de Priester W., Lugtenberg B.J.J.,
RT Bloembergen G.V.;
RT "Involvement of type 4 pili of Pseudomonas fluorescens in tomato root
colonization.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
CC -1 SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS (BY
SIMILARITY).
CC -1 SIMILARITY: BELONGS TO THE FIMBRIAL PROTEIN (N-ME-PHE)PILIN
FAMILY.
DR EMBL: AF297457; AAG18586.1;
DR InterPro: IPR002416; Bac_GSPH.
DR InterPro: IPR001082; Pilin.
DR InterPro: IPR001120; Prok_N_methyltn.
DR Pfam: PF00114; pilin; 1.
DR PRINTS: PR00885; BCTERIALGSPH.
DR PRODOM: PD000666; pilin; 1.
DR PROSITE: PS00409; PROKAR_NTER_METHYL; 1.
KW Fimbria; Methylation.
SEQUENCE 140 AA; 14077 MW; 3299B0751C6603C4 CRC64;

Query Match 20.5%; Score 129.5; DB 2; Length 140;
Best Local Similarity 33.6%; Pred. No. 0.00015;
Matches 38; Conservative 19; Mismatches 41; Indels 15; Gaps 4;

QY 8 ARSEASALASVNPDKTYEALSRGWSVKS-GTGEDATKKEVPLGVAADANKLGTAL 67
DB 35 ARAKVIYGLAEASSLKVPEDLTKGTSPTAAN-----TGVPSNNC-TMSVS 82
QY 68 PPDADGTADITLFTMGAGPKNKGIITLRTAADLMKCTSDODEQFIPKGC 120
DB 83 GDATAGTA--TVCAIKAEAPSSIVGKTITLSR-AGTGVSSCSNVAEEPLPAG 132
RESULT 4
Q56799 PRELIMINARY; PRT: 136 AA.
AC Q56799:
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE FIMBRILIN.
GN FIMA.
OS Xanthomonas campestris.
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
CC Xanthomonas.
OX NCBI_Taxid=339;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3240 (NCPB);
RX MEDLINE=97175558; PubMed=9023213;
RA Ojaneen-Reus T., Kalkkinen N., Westerlund-wikstrom B., van Doorn J.,
RA Hahtela K., Niemeläho-Iassila E.L., Wengelnik K., Bonas U.,
RA Korhonen T.K.;

RT "Characterization of the *fimA* gene encoding bundle-forming fimbriae of
RT the plant pathogen *Xanthomonas campestris* pv. *vesicatoria*.";
RL J. Bacteriol. 179:1280-1290(1997).

DR ProdOm; PD000666; P1lin; 1.
SQ SEQUENCE 136 AA; 14302 MW; A834A9C4EA7C63B1 CRC64;

Query Match	20.0%;	Score 126.5;	DB 2;	Length 136;
Best Local Similarity	32.5%;	Pred. NO. 0.00028;		
Matches 37;	Conservative 18;	Mismatches 44;	Indels 15;	Gaps 4;

```
OY      8 AREEGSAALASVPLTFTTYEALISGWSVMSGTGEEDTKREVLGAQAANLGLTALK 67
        | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db     35 AKSQVTAGLAINEPKQTQYEVALNBS-----KTVADITE-----LGKSPSECTIAPTIT 85

OY      68 PDDADGTADDTLTFTMGSGPRKNRKIIITLTRTADGIMKTSSPDSDQFLPKGC 121
        | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db     86 ALSTGTIGETCL-----GNTGVCKRKYTLIR-ANDGWTCRTKLALKVPACG 133
```

RESULT	5	PRELIMINARY;	PRT;	147 AA.
030583				
ID	030583			
AC	030583			
DT	01-JAN-1998	(TREMblrel. 05		Created)
DT	01-JAN-1998	(TREMblrel. 05		Last sequence update)
DT	01-JUN-2001	(TREMblrel. 17,		Last annotation update)

0C	Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
0C	Acinetobacter.
0X	NCBI_TaxID=471;

RP SEQUENCE FROM N.A.
RC STRAIN-BD413.
RX MEDLINE=98027349; PubMed=9361398;
RA Porstendoerfer D., Drotschmann U., Aaverhoff B.,
RT "A novel cloning gene, comp., is essential for natural
RL transformation of *Acinetobacter* sp. strain BD413.";
BL Appl. Environ. Microbiol. 63:4150-4157(1997).

CC -1- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
CC NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
CC CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
CC CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS (BY
CC SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE FIMBRIAL PROTEIN (N-ME-PHE)PILIN

CC -1- SIMILARITY: BELONGS TO THE FIMBRIAL PROTEIN (N-ME-PHE).PILIN
CC FAMILY.
DR HSSL; AF012550; AAC45886.1; -.
DR EMBL; P02974; 2PIL.
DR InterPro; IPR001082; PILin.
DR InterPro; IPR001120; Prok_N_methyltn.
DR Pfam; PF00114; PILin; 1.
DR PROSITE; PD000666; PILAR; 1.
DR PROSITE; PS00409; PROKAR_NTER_METHYL; 1.
KW Fimbria; methylation.
FT MOD_RS 7 METHYLATION (BY SIMILARITY).
SQ SEQUENCE 147 AA; 14872 MW; 682DBC062230C479 CRC64;

Query Match	18.5%;	Score 117;	DB 2;	Length 147;
Best Local Similarity	30.2%;	Pred. No. 0.0022;		
Matches	38;	Conservative	17;	Mismatches 37;
				Indels 34;
				Gaps 6

```
OY      SEGSLALSNVPLRTTVEALSRCGNSVKSG-----GTEDATKREYPLIGA---AD   57
          10 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      SEGLTAAS---MTVTSENTLNAGALVAGPPSTAGSSCVGVDDISASMTTNVAITATCG 96
          40 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      ANKLGTIALKPDPDCTADITLTFTMGAGAGKNKGKIITLTLRTAAD--LMKCTSDDEQ 115
          58 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

Db 97 ASSAGQIIV-----TMDT-----KAKGANITLTPTYASGAVTWKCTTSDK 139

QY 116 FIPKGC 121

Db 140 YVPSEC 145

RESULT	6
052613	

DT	01-JUN-1998	(TREMBlurel. 06, Created)
DT	01-JUN-1998	(TREMBlurel. 06, last sequence update)
DT	01-JUN-2001	(TREMBlurel. 17, last annotation update)

OC	Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group.
OC	Xanthomonas.
OX	NCBI_TaxID=346;

Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases

CC -1- SUBUNIT: THE FILLI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
CC NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
CC CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
CC CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED FILUS (BY
CC SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE FIMBRIAL PROTEIN (N-ME-PHF)PILIN

CC -1- SIMILARITY: BELONGS TO THE FIBRILLAR PROTEIN (N-ME-PHE)PILIN
CC FAMILY.
DR EMBL: AF042829; ABA97527.1; -.
DR InterPro: IPR001082; PiliIn.
DR InterPro: IPR001120; Prok_N_methylIn.
DR Pfam: PF00114; PiliIn. 1.
DR ProDom: PD000665; PiliIn. 1.
DR ProSITE: PS00409; PROKAR_NTER_METHYL. 1.
KW Fimbrin; Methylation.
KW MOD_RES 7 METHYLATION (BY SIMILARITY).
SQ SEQUENCE 146 AA; 15249 MW; 6D0CF3CEB24ADE CRC64;

Query Match	18.3%	Score 115.5	DB 2	Length 146
Best Local Similarity	31.1%	Pred. No. 0.003		
Matches 37	Conservative 17	Mismatches 52	Indels 13	Gaps 5

[illegible]

RESULT	7	
Q9APK5		
ID	Q9APK5	PRELIMINARY;
		PRT; 145 AA

DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, last annotation update)
DE FIMA PRECURSOR.
OS *Xanthomonas hyacinthi*.
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group

OX NCBI_TaxID=56455;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=115722;
RA van Doorn J.J., Hollinger T.C., Oudega B.;
RT "Analysis of the Type IV Fimbrial-Subunit Gene flmA of Xanthomonas

RT Hyacinth: Application in PCR-Mediated Detection of Yellow Disease in
 RT Hyacinth: " "
 RL Appl. Environ. Microbiol. 67:596-607 (2001).
 DR EMBL: AF281159; AAK11163.1; "
 SO SEQUENCE 145 AA; 14911 MW; BB521BA0B59D68E1 CRC64;

Query Match 17.7%; Score 111.5; DB 2; Length 145;
 Best Local Similarity 31.1%; Pred. No. 0.007; Mismatches 43; Indels 19; Gaps 6;
 Matches 37; Conservative 20; Mismatches 43; Indels 19; Gaps 6;

QY 8 ARSEGASALASVPLKTYVEALSR-----GWSVKS-----GNGEDATKKEVPL 52
 DB 35 AKQVSGALAEITPGVQAEIRAEKAV-----TTGADVGLQASISRCG-1A5S 84
 QY 68 PDPADGTADITLFTMGAGAPKNGKITLTETA-----ADLMCTSDODEQPIPKGC 121
 DB 85 VDPG-GAA--TLCTLKGNAGIN-GOTIOWTRAADTANGTGWCTTAAVEKLRPATC 139

RESULT 8
 09S4E2 PRELIMINARY; PRT; 130 AA.
 AC 09S4E2;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE FIMBRIAL SUBUNIT (FRAGMENT).
 GN FIMA.
 OS Bacteroides nodosus (Dichelobacter nodosus).
 OC Bacteria; Proteobacteria; gamma subdivision; Cardiolobacteriaceae;
 OC Dichelobacter.
 OX NCBI_TaxID=870;
 [1]
 RP SEQUENCE FROM N.A.
 RA Zhou H., Hickford J.G.H.;
 RT "Dichelobacter nodosus fimbrial subunit gene (fima).";
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Zhou H., Hickford J.G.H.;
 RT "Dichelobacter nodosus fimbrial subunit gene. "
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF146890; AAD43087.1; "
 DR EMBL: AF316611; AAK00324.1; "
 DR InterPro: IPR001082; Piliin;
 DR Pfam: PF00114; Piliin; 1.
 DR ProDom: PD000666; Piliin; 1.
 FT NON_TER 1
 SO SEQUENCE 130 AA; 13838 MW; 0978D2488FEA6C9D CRC64;

Query Match 17.5%; Score 110.5; DB 2; Length 130;
 Best Local Similarity 27.8%; Pred. No. 0.0076;
 Matches 37; Conservative 22; Mismatches 45; Indels 29; Gaps 7;

QY 8 ARSEGASALASVPLKTYVEALSR-----GWSVKS-----GNGEDATKKEVPL 52
 DB 10 ASQVSRVSEETGMRITETCLDGRKDCPTGWTSTNLLAAGSSTNNAT----- 63
 QY 53 GVAADANKLG-TIALKPDADGTADITLFTMG-GAGPKNGKITLTTRTAAGLMKCTS 110
 DB 64 --ADPGGGGINIAY--ALSTAKNTKEATFFGONAAATLHGKLTWTR-SPEATMSCSR 117
 QY 111 DODEQFIKGCGR 123
 DB 118 DVDERFKPTGCKK 130

RESULT 9
 09X4G7 PRELIMINARY; PRT; 153 AA.
 AC 09X4G7;

DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE TYPE IV-A PILIN PRECURSOR PILA.
 GN PILA.
 OS Vibrio cholerae.
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
 OX NCBI_TaxID=666;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=99150277; PubMed=10024587;
 RA Fullner K.J., Mekalanos J.J.;
 RT "Genetic characterization of a new type IV-A pilus gene cluster found
 in both classical and El Tor biotypes of Vibrio cholerae.";
 RL Infect. Immun. 67:1393-1404 (1999).
 CC - FUNCTION: INVOLVED IN A GENERAL SECRETION PATHWAY (GSP) FOR THE
 EXPORT OF PROTEINS (BY SIMILARITY).
 CC - SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
 NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
 CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
 CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS (BY
 SIMILARITY).
 CC - SIMILARITY: BELONGS TO THE FIMBRIAL PROTEIN (N-WE-PHE)PILIN
 FAMILY.
 CC - SIMILARITY: TO BACTERIAL GENERAL SECRETION PATHWAY PROTEIN G
 (PULG/OUTG/XPSG/EXEG/XCPT) FAMILY.
 DR EMBL: AF109904; AAD21029.1; "
 DR InterPro: IPR000983; Bac_GSPG.
 DR InterPro: IPR002416; Bac_GSPH.
 DR InterPro: IPR001082; Piliin.
 DR InterPro: IPR001120; Prok_N_methylen.
 DR Pfam: PF00114; Piliin; 1.
 DR PRINTS: PR00813; BCTERIALGSPG.
 DR PRINTS: PR00885; BCTERIALGSPH.
 DR ProDom: PD000666; Piliin; 1.
 DR PROSITE: PS00409; PROKAR_NTER_METHYL; 1.
 KW Fimbria; Methylation; Transport.
 FT MOD_RES 12
 SO SEQUENCE 153 AA; 15722 MW; 84681B115DE95A22 CRC64;

Query Match 17.4%; Score 109.5; DB 2; Length 153;
 Best Local Similarity 31.0%; Pred. No. 0.011;
 Matches 36; Conservative 17; Mismatches 38; Indels 25; Gaps 6;

QY 16 LASVNPDKTYVEALSRGWSVSGTGEDATKKEVPLGVAADANKLGITAKPDADGTA 75
 DB 48 LANITAKNTINEDYATGESFPATTA-----GTAGFTRLGTV--EDMGGKRI 93
 QY 76 DI--TLFTMG-----AGPKNGKITLTTRTAAGLMKCTSDODEQPIPKGCS 122
 DB 94 VIAPIASGALGSTITYTTDPAGVSSK-TOLARD-ANGLIMCTSTYVSELAPKCT 147

RESULT 10
 09KPE5 PRELIMINARY; PRT; 167 AA.
 AC 09KPE5;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE FIMBRIAL PROTEIN.
 GN VC2423.
 OS Vibrio cholerae.
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
 OX NCBI_TaxID=666;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EL TOR N16961 / SEROTYPE O1;
 RX MEDLINE=20406833; PubMed=10952301;
 RA Heidelberg J.F., Eissen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,
 RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
 RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

RA Ermolova M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
 RA McDonald L., Utterback T., Fleishman R.D., Niernan W.C., White O.,
 RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
 RA Fraser C.M.;
 RT "DNA sequence of both chromosomes of the cholera pathogen *Vibrio*
 RT *cholerae*";
 RL Nature 406:477-483(2000).
 CC -1- FUNCTION: INVOLVED IN A GENERAL SECRETION PATHWAY (GSP) FOR THE
 CC EXPORT OF PROTEINS (BY SIMILARITY).
 CC -1- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
 CC NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
 CC CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
 CC CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE FIMBRIAL PROTEIN (N-ME-PHE)PILIN
 CC FAMILY.
 CC -1- SIMILARITY: TO BACTERIAL GENERAL SECRETION PATHWAY PROTEIN G
 CC (PULG/OUNG/XPSG/XEGS/XCPT) FAMILY.
 CC EMBL; AE004312; AAF95566.1; .
 DR TIGR; VC2423; .
 DR InterPro: IPR000983; Bac_GSPG.
 DR InterPro: IPR002416; Bac_GSPH.
 DR InterPro: IPR001082; Pilin.
 DR InterPro: IPR001120; Prok_N_methyltn.
 DR Pfam: PF00114; pilin; 1.
 DR PRINTS: PR00813; BCTERIALGSPG.
 DR PRINTS: PR00885; BCTERIALGSPH.
 DR PRODOM: PD000666; Pilin; 1.
 DR PROSITE: PS00409; PROKAR_NTER_METHYL; 1.
 KW Complete proteome: Fimbrin; Methylation; Transport.
 SQ SEQUENCE 167 AA; 17266 MW; 4C0CAB115AC677F CRC64;

Query Match 17.4%; Score 109.5; DB 2; Length 167;
 Best Local Similarity 31.0%; Pred. No. 0.012;
 Matches 36; Conservative 17; Mismatches 38; Indels 25; Gaps 6;

OY 16 LASVPLKTYVEALSRGWSVSGTGEDATKKEVPLGVADANKLGITALKPPADGTA 75
 DB 62 LANITALKTIEDYIATGCSFPATTA-----GTAACTFRTGTV--EDMGDSKI 107
 OY 76 DI-TLFTFMG-----AGPKNGKGIITLRTAADGLMKTSDODEFIRKGS 122
 DB 108 VIAPLASGALGCTIKYTFDAGVSSK-IQLARD-ANGLMCTSTVTSEIAPKGT 161

RESULT 11
 O9PAH6 PRELIMINARY: PRT: 148 AA.
 AC O9PAH6: 01-OCT-2000 (TREMBlrel. 15; Created)
 DT 01-OCT-2000 (TREMBlrel. 15; Last sequence update)
 DE 01-JUN-2001 (TREMBlrel. 17; Last annotation update)
 GN XP2542.
 OS *Xylella fastidiosa*.
 OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
 OC *Xylella*.
 OX NCBI_TaxID=2371;
 RP SEQUENCE FROM N.A.
 RC STRAIN-9A5C;
 RX MEDLINE=20365717; PubMed=10910347;
 RA Simpson A.J.G., Rehnach F.C., Artuda P., Abreu F.A., Acencio M.,
 RA Alvarenga R., Alves L.M.C., Araya J.E., Bala G.S., Baptista C.S.,
 RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
 RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carer H.,
 RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto G.M.,
 RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
 RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
 RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
 RA Garier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
 RA Ho P.L., Hohnselt J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,

RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
 RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
 RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
 RA Machado M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
 RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
 RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Neto L.E.S.,
 RA Nham A.J., Nobrega F.G., Nunes L.R., Oliveira M.A.,
 RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
 RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
 RA Queiroz M.V., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
 RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
 RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
 RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
 RA de Souza A.P., Terenzi M.F., Trufi D., Tsai S.M., Tshahko M.H.,
 RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
 RT "The genome sequence of the plant pathogen *Xylella fastidiosa*";
 RL Nature 406:151-159(2000).
 CC -1- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
 CC NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
 CC CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
 CC CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE FIMBRIAL PROTEIN (N-ME-PHE)PILIN
 CC FAMILY.
 CC EMBL; AE004061; AAF85339.1; .
 DR InterPro: IPR002416; Bac_GSPH.
 DR InterPro: IPR001082; Pilin.
 DR InterPro: IPR001120; Prok_N_methyltn.
 DR Pfam: PF00114; pilin; 1.
 DR PRINTS: PR00885; BCTERIALGSPH.
 DR PRODOM: PD000666; Pilin; 1.
 DR PROSITE: PS00409; PROKAR_NTER_METHYL; 1.
 KW Complete proteome: Fimbrin; Methylation.
 SQ SEQUENCE 148 AA; 15034 MW; F17C024F2716ED5 CRC64;

Query Match 17.3%; Score 109; DB 2; Length 148;
 Best Local Similarity 29.6%; Pred. No. 0.012;
 Matches 37; Conservative 15; Mismatches 49; Indels 24; Gaps 4;

OY 8 ARSEASALASVNPDKTYVEALSRGWSVSGTGEDATKKEVPLGVADANKLGITALK 67
 DB 35 ARSQIAALAEITPPKVGQAEIRIADG-----QAATPNAIGLRAPTRCGTIYVD 84
 OY 68 PDPADGTADITLFTFMGAGAPKNGKGIITLRTA-----ADGLMKTSDODEOFI 117
 DB 85 IAPSAASA---ITCTMIGNAGVN-NQITLRTIADNNMGQGVGNMTCTTAPALVT 140
 OY 118 PKGCS 122
 DB 141 PAGCT 145
 RESULT 12
 Q59794 PRELIMINARY: PRT: 154 AA.
 AC Q59794: 01-JUN-1998 (TREMBlrel. 06; Created)
 DT 01-JUN-1998 (TREMBlrel. 06; Last sequence update)
 DE 01-JUN-2001 (TREMBlrel. 17; Last annotation update)
 GN FIMBRIAL PROTEIN PRECURSOR (PILIN) (STRAIN 577B).
 OS *Pseudomonas aeruginosa*.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC *Pseudomonas*.
 OX NCBI_TaxID=287;
 RP SEQUENCE FROM N.A.
 RC STRAIN-577B;
 RX MEDLINE=94131566; PubMed=7507890;
 RA Castic P.A., Deal C.D.;
 RT "Differentiation of *Pseudomonas aeruginosa* pill based on sequence and

RT B-cell epitope analyses.
 RL Infect. Immun. 62:371-376(1994).
 CC -1- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
 CC NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH. THEY
 CC CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
 CC CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.
 CC -1- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
 DR EMBL: S68101; AAC60461.1; .
 DR HSSP: P02974; 2PIL.
 DR Interpro: IPR001082; PiliN.
 DR Pfam: PF00114; PiliN; 1.
 DR ProDom: PD000666; PiliN; 1.
 DR PROSITE: PS00409; PROKAR_NTER.METHYL; 1.
 KW Fimbria; Methylation.
 FT CHAIN 1 154 FIMBRIAL PROTEIN.
 FT DISULFID 133 151 BY SIMILARITY.
 FT MOD_RES 7 7 METHYLATION (BY SIMILARITY).
 SQ SEQUENCE 154 AA; 16317 MW; 52A0A56725135719 CRC64;

Query Match 16.7%; Score 105.5; DB 2; Length 154;
 Best Local Similarity 28.5%; Pred. No. 0.026; Mismatches 52; Indels 11; Gaps 6;
 Matches 35; Conservative 25;

OY 8 ANSEGASALASVNPILKTYEALSRGWSVSGTGEDATKREYPLGVADANKLTIALK 67
 DB 35 ARTQVTRAVSEVSAIKTAESAILEKEITVS-TKTPNDQYDIDGTFESLLDLKGEQIK 93
 OY 68 -IDPADGTADITLTFMG-ACPKNGKITITLTATADGLMKCTSDQ-----DEQIFPKG 120
 DB 94 VTDNKNKT--VOLVATLGGSSSAIKGAVITVSRD-AGQVSCNITKPTANKPNYAPAN 150
 OY 121 CSR 123
 DB 151 CKR 153

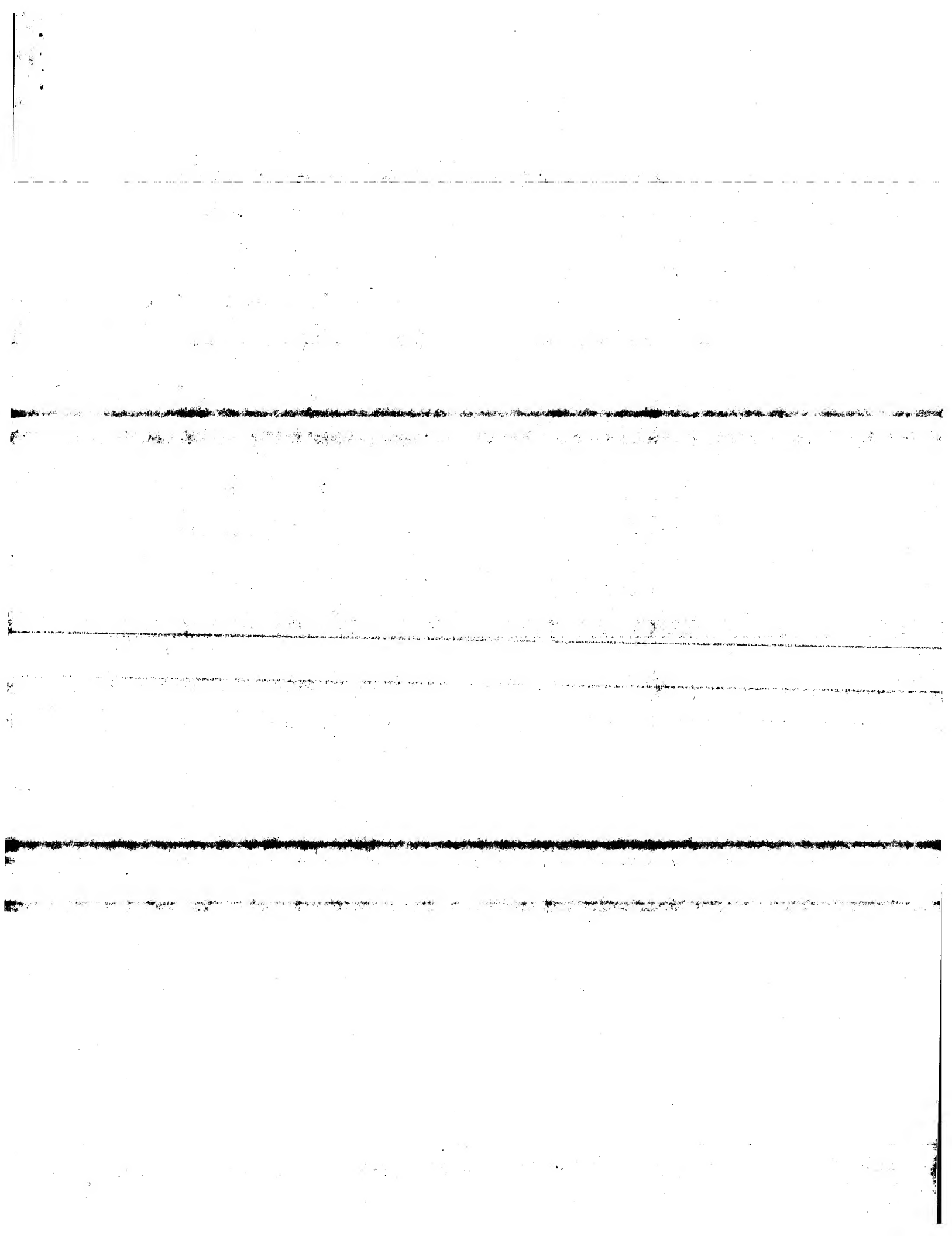
RESULT 13
 ID 060163 PRELIMINARY; PRT; 159 AA.
 AC 060163
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE PREPILIN.
 OS Moraxella bovis.
 CC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae; Moraxella.
 CX NCBI_TaxID=476;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-R593L / SEROTYPE D;
 RA MEDLINE=94327452; PubMed=8051000;
 RA Atwell J.L., Tennent J.M., Lepper A.W., Ellemann T.C.;
 RT "Characterization of pili genes from seven serologically defined
 RT prototype strains of Moraxella bovis."
 RL J. Bacteriol. 176:4875-4882(1994).
 CC -1- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
 CC NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH. THEY
 CC CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
 CC CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE FIMBRIAL PROTEIN (N-ME-PHE)PILIN
 CC FAMILY.
 DR EMBL: L32971; AAA53563.1; .
 DR EMBL: L32970; AAA53562.1; .
 DR Interpro: IPR001082; PiliN.
 DR Interpro: IPR001120; ProK_N.methyln.
 DR Pfam: PF00114; PiliN; 1.
 DR ProDom: PD000666; PiliN; 1.
 DR PROSITE: PS00409; PROKAR_NTER.METHYL; 1.
 KW Fimbria; Methylation.

FT MOD_RES 7 7 METHYLATION (BY SIMILARITY).
 SQ SEQUENCE 159 AA; 16459 MW; F2113DD7ECD578FC CRC64;

Query Match 16.5%; Score 104; DB 2; Length 159;
 Best Local Similarity 25.8%; Pred. No. 0.037; Mismatches 58; Indels 10; Gaps 3;
 Matches 32; Conservative 24;

OY 8 ANSEGASALASVNPILKTYEALSRGWSVSGTGEDATKREYPLGVAD--ANKLGTI 64
 DB 35 SKSQTRRVVGLAAGKTAVDALLFEGKEPEVLQANNADTSKEDIGLDTSNKPRSNLSNV 94
 OY 65 ALKPPDAGTADITLTFMGAGCPKNGKITITLTATADGLMKCTSDQ-----EQIFP 118
 DB 95 ELGGSATISAG-TITGTLGTANKDITGAKIMQNPADGVNCTTIDGSAATGMRKDFIP 153
 OY 119 KCOS 122
 DB 154 TGCT 157

RESULT 14
 ID 09PAH9 PRELIMINARY; PRT; 148 AA.
 AC 09PAH9
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE FIMBRIAL PROTEIN.
 GN XF2539.
 OS Xylella fastidiosa.
 CC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
 CC Xylella.
 CX NCBI_TaxID=2371;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-9A5C;
 RA MEDLINE=20365717; PubMed=10910347;
 RA Simpson A.J.G., Rehnach F.C., Arruda P., Abreu F.A., Acencio M.,
 RA Alvaerenga R., Alves L.M.C., Araya J.E., Bala G.S., Baptista C.S.,
 RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
 RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrier H.,
 RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
 RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Porri H.,
 RA Facinoni A.P., Ferreira A.J.S., Ferreira V.C.A., Fetto J.A.,
 RA Fraga J.S., Franca S.C., Franco M.C., Froime M., Furian L.R.,
 RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
 RA Ho P.L., Hohlseisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
 RA Krieger J.E., Kuranae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
 RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
 RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
 RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsushima A.T.,
 RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
 RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
 RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
 RA de Oliveira M.C., de Oliveira R.C., Palmeira D.A., Paris A.,
 RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
 RA Quagho R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
 RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
 RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
 RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
 RA de Souza A.P., Terezi M.F., Truffi D., Tsai S.M., Tsubako M.H.,
 RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
 RA Zago M.A., Zait M., Meidanis J., Setubal J.C.,
 RT "The genome sequence of the plant pathogen Xylella fastidiosa."
 RL Nature 406:151-159(2000).
 DR EMBL: AE004061; AAF85336.1; .
 DR Interpro: IPR002416; Bac_GSPH.
 DR Interpro: IPR001082; PiliN.
 DR Pfam: PF00114; PiliN; 1.
 DR PRINTS: PR00885; BCTERIALGSPH.
 DR ProDom: PD000666; PiliN; 1.
 KW Complete proteome.



GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 8, 2002, 15:23:15 ; Search time 32.48 Seconds
(without alignments)
85.219 Million cell updates/sec

Title: US-09-865-159-4

Perfect score: 631
Sequence: 1 ALEGTFRARSGASALASVN.....GLMKTSDDEQFIRKCSR 123

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents,AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCRUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	99.5	15.8	154	US-08-486-099-108	Sequence 108, App
2	99.5	15.8	154	US-08-360-107A-118	Sequence 118, App
3	99.5	15.8	154	US-08-484-223B-108	Sequence 108, App
4	99.5	15.8	154	US-08-919-597-108	Sequence 108, App
5	99.5	15.8	154	US-08-475-668A-108	Sequence 108, App
6	99.5	15.8	154	US-08-485-551A-108	Sequence 108, App
7	99.5	15.8	154	US-08-471-913A-108	Sequence 108, App
8	99.5	15.8	154	US-08-485-264A-108	Sequence 108, App
9	96	15.2	17	US-07-638-492-2	Sequence 2, Appli
10	93	14.7	17	US-08-084-739-5	Sequence 5, Appli
11	93	14.7	17	US-07-638-492-1	Sequence 1, Appli
12	93	14.7	17	US-08-260-199A-1	Sequence 1, Appli
13	91	14.4	16	5445818-10	Patent No. 5445818
14	86	13.6	17	US-08-194-290-8	Sequence 8, Appli
15	86	13.6	17	US-08-614-377A-8	Sequence 8, Appli
16	86	13.6	17	US-09-142-648B-8	Sequence 8, Appli
17	82	13.0	14	US-08-084-739-3	Sequence 3, Appli
18	82	13.0	14	5445818-2	Patent No. 5445818
19	73	11.6	19	US-08-409-995-4	Sequence 4, Appli
20	73	11.6	19	US-08-685-467-4	Sequence 4, Appli
21	73	11.6	2353	US-09-377-155-33	Sequence 33, Appli
22	73	11.6	2353	US-08-913-942-4	Sequence 4, Appli
23	69.5	11.0	520	US-09-000-016-7	Sequence 7, Appli
24	69.5	11.0	734	US-09-000-016-4	Sequence 4, Appli
25	69.5	11.0	823	US-09-000-016-2	Sequence 2, Appli
26	69	10.9	17	US-08-084-739-10	Sequence 10, Appli
27	69	10.9	18	US-07-638-492-4	Sequence 4, Appli

28	69	10.9	563	2	US-08-714-168-1	Sequence 1, Appli
29	69	10.9	563	4	US-09-320-721A-1	Sequence 1, Appli
30	67	10.6	294	1	US-08-137-175A-9	Sequence 9, Appli
31	67	10.6	294	4	US-08-479-017-9	Sequence 9, Appli
32	66	10.5	679	4	US-08-913-942-15	Sequence 15, Appli
33	65	10.3	383	4	US-09-206-800-7	Sequence 7, Appli
34	65	10.3	921	4	US-09-206-800-10	Sequence 10, Appli
35	65	10.3	1167	2	US-08-589-756-2	Sequence 2, Appli
36	65	10.3	1167	4	US-09-206-800-2	Sequence 2, Appli
37	65	10.2	1313	2	US-08-244-537-2	Sequence 2, Appli
38	64.5	10.2	262	4	US-09-363-189B-6	Sequence 6, Appli
39	64	10.1	2123	4	US-08-968-685A-10	Sequence 10, Appli
40	63.5	10.1	344	1	US-08-400-422-4	Sequence 4, Appli
41	63.5	10.1	725	2	US-08-816-105A-1	Sequence 1, Appli
42	62.5	9.9	286	1	US-08-872-784-3	Sequence 3, Appli
43	62.5	9.9	286	2	US-09-100-851-3	Sequence 3, Appli
44	62.5	9.9	286	4	US-09-265-294-3	Sequence 3, Appli
45	62.5	9.9	393	3	US-09-127-124-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-08-486-099-108

Sequence 108, Application US/08486099

Patent No. 6013263

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Mathews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteaway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF

TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS

NUMBER OF SEQUENCES: 209

CORRESPONDENCE ADDRESS: 209

ADDRESS: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/486, 099

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-031

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 108:

SEQUENCE CHARACTERISTICS:

LENGTH: 154 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-08-486-099-108

Query Match 15.8%; Score 99.5; DB 3; Length 154;
 Best Local Similarity 27.6%; Pred. No. 0.00028;
 Matches 35; Conservative 22; Mismatches 51; Indels 19; Gaps 7;

QY 8 ARSEGASALASVNPDKTVEEALSRGWSVKSQTGTEDATKKEVPLGVADANKL-----GT 63
 DB 35 ARQVTRAVSEVSAIKTAESAILEGKEIYS-----SATPRDQYDIOGFTSTLLDSSGK 89

QY 64 IALK-PDPADGTADITLFTFMG-GAGPKNKGKIIITLRTAADGLMKCTSDQ-----DEQF 116
 DB 90 SQIOVTDNDGT--VELVATLKGSSGSAIKGAVITVSR-KNDGVWNCKITKPTAMKPNY 146

QY 117 IPKCSR 123
 DB 147 APANCPK 153

RESULT 2

US-08-360-107A-118
 Sequence 118, Application US/08360107A
 Patent No. 6017536

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.
 APPLICANT: Matthews, Thomas J.
 APPLICANT: Wild, Carl T.
 APPLICANT: Barney, Shawn O.
 APPLICANT: Lambert, Dennis M.
 APPLICANT: Pelletway, Stephen R.
 APPLICANT: Langlois, Alphonse J.
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
 TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
 NUMBER OF SEQUENCES: 149
 CORRESPONDENCE ADDRESSES:
 ADDRESS: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/360,107A
 FILING DATE: 20-DEC-1994
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.
 REGISTRATION NUMBER: 30,742
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-9741/8864
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-9741/8864

INFORMATION FOR SEQ ID NO: 118:

SEQUENCE CHARACTERISTICS:
 LENGTH: 154 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 US-08-360-107A-118

Query Match 15.8%; Score 99.5; DB 3; Length 154;
 Best Local Similarity 27.6%; Pred. No. 0.00028;
 Matches 35; Conservative 22; Mismatches 51; Indels 19; Gaps 7;

QY 8 ARSEGASALASVNPDKTVEEALSRGWSVKSQTGTEDATKKEVPLGVADANKL-----GT 63
 DB 35 ARQVTRAVSEVSAIKTAESAILEGKEIYS-----SATPRDQYDIOGFTSTLLDSSGK 89

DB 35 ARQVTRAVSEVSAIKTAESAILEGKEIYS-----SATPRDQYDIOGFTSTLLDSSGK 89

QY 64 IALK-PDPADGTADITLFTFMG-GAGPKNKGKIIITLRTAADGLMKCTSDQ-----DEQF 116
 DB 90 SQIOVTDNDGT--VELVATLKGSSGSAIKGAVITVSR-KNDGVWNCKITKPTAMKPNY 146

QY 117 IPKCSR 123
 DB 147 APANCPK 153

RESULT 3

US-08-484-223B-108
 Sequence 108, Application US/08484223B
 Patent No. 6020459

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.
 APPLICANT: Matthews, Thomas J.
 APPLICANT: Wild, Carl T.
 APPLICANT: Barney, Shawn O.
 APPLICANT: Lambert, Dennis M.
 APPLICANT: Pelletway, Stephen R.
 APPLICANT: Langlois, Alphonse J.
 TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
 TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
 NUMBER OF SEQUENCES: 245
 CORRESPONDENCE ADDRESSES:
 ADDRESS: Pennie & Edmonds LLP
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/484,223B
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.
 REGISTRATION NUMBER: 30,742
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-9741/8864
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-9741/8864

INFORMATION FOR SEQ ID NO: 108:

SEQUENCE CHARACTERISTICS:
 LENGTH: 154 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 US-08-484-223B-108

Query Match 15.8%; Score 99.5; DB 3; Length 154;
 Best Local Similarity 27.6%; Pred. No. 0.00028;
 Matches 35; Conservative 22; Mismatches 51; Indels 19; Gaps 7;

QY 8 ARSEGASALASVNPDKTVEEALSRGWSVKSQTGTEDATKKEVPLGVADANKL-----GT 63
 DB 35 ARQVTRAVSEVSAIKTAESAILEGKEIYS-----SATPRDQYDIOGFTSTLLDSSGK 89

QY 64 IALK-PDPADGTADITLFTFMG-GAGPKNKGKIIITLRTAADGLMKCTSDQ-----DEQF 116
 DB 90 SQIOVTDNDGT--VELVATLKGSSGSAIKGAVITVSR-KNDGVWNCKITKPTAMKPNY 146

OY 117 IPKCSR 123
DB 147 APANCPK 153

RESULT 4

US-08-919-597-108
Sequence 108, Application US/08919597
Patent No. 6054265
GENERAL INFORMATION:
APPLICANT: Bolognesi, Danl P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Peteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/919,597
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/470,896
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 154 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-919-597-108

Query Match 15.8%, Score 99.5; DB 3; Length 154;
Best Local Similarity 27.6%, Pred. No. 0.00028;
Matches 35; Conservative 22; Mismatches 51; Indels 19; Gaps 7;

OY 8 ARSEGASALASVNP...GT 63
DB 35 ARTQYTRAVSEVSA...GT 89
OY 64 IALK-PDPADGTADIT...DEOF 116
DB 90 SOIQVTDMDGT--VELVATLTKSSGSAIKGAVITVSR-KNDGVNCKITTKPTAMKPNY 146
OY 117 IPKCSR 123
DB 147 APANCPK 153

RESULT 5

US-08-475-668A-108
Sequence 108, Application US/08475668A
Patent No. 6060065
GENERAL INFORMATION:
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Peteway, Stephen R.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,668A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 154 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-475-668A-108

Query Match 15.8%, Score 99.5; DB 3; Length 154;
Best Local Similarity 27.6%, Pred. No. 0.00028;
Matches 35; Conservative 22; Mismatches 51; Indels 19; Gaps 7;

OY 8 ARSEGASALASVNP...GT 63
DB 35 ARTQYTRAVSEVSA...GT 89
OY 64 IALK-PDPADGTADIT...DEOF 116
DB 90 SOIQVTDMDGT--VELVATLTKSSGSAIKGAVITVSR-KNDGVNCKITTKPTAMKPNY 146
OY 117 IPKCSR 123
DB 147 APANCPK 153
RESULT 6
US-08-485-551A-108
Sequence 108, Application US/08485551A
Patent No. 6068973
GENERAL INFORMATION:
APPLICANT: Bolognesi, Danl P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Peteway, Stephen R.
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,551A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-023
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 154 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-485-551A-108

Query Match 15.8%; Score 99.5; DB 3; Length 154;
Best Local Similarity 27.6%; Pred. No. 0.00028;
Matches 35; Conservative 22; Mismatches 51; Indels 19; Gaps 7;

QY 8 ARSEGASALASVNPDKTVEEALSRGWSVKSQTGTEADTKKEVPLGVAADANKL-----GT 63
DB 35 ARTQVTRAVSEVSAKTAESAILEGKEIYS-----SATPKDTQYDIGFTSTLIDSGSK 89
QY 64 IALK-PDPADGTADITLFTMG-GAGPRNKGKIIITLRTAADGLMKCTSDQ-----DEOF 116
DB 90 SGIQVTDNODGT--VELVATLIGKSSGSAIKGAVITVSR-KNDGWNCKITKTPAMKPNY 146
QY 117 IPKGCGR 123
DB 147 APANCPK 153

RESULT 7
US-08-471-913A-108
Sequence 108, Application US/08471913A
Patent No. 6093794
GENERAL INFORMATION:
APPLICANT: Biolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Peteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS

TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 214
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,913A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 154 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-471-913A-108

Query Match 15.8%; Score 99.5; DB 3; Length 154;
Best Local Similarity 27.6%; Pred. No. 0.00028;
Matches 35; Conservative 22; Mismatches 51; Indels 19; Gaps 7;

QY 8 ARSEGASALASVNPDKTVEEALSRGWSVKSQTGTEADTKKEVPLGVAADANKL-----GT 63
DB 35 ARTQVTRAVSEVSAKTAESAILEGKEIYS-----SATPKDTQYDIGFTSTLIDSGSK 89
QY 64 IALK-PDPADGTADITLFTMG-GAGPRNKGKIIITLRTAADGLMKCTSDQ-----DEOF 116
DB 90 SGIQVTDNODGT--VELVATLIGKSSGSAIKGAVITVSR-KNDGWNCKITKTPAMKPNY 146
QY 117 IPKGCGR 123
DB 147 APANCPK 153

RESULT 8
US-08-485-264A-108
Sequence 108, Application US/08485264A
Patent No. 6228983
GENERAL INFORMATION:
APPLICANT: Biolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Peteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING
NUMBER OF SEQUENCES: 232
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York

STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,264A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-021
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 154 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-485-264A-108

Query Match 15.8%; Score 99.5; DB 4; Length 154;
Best Local Similarity 27.6%; Pred. No. 0.00028;
Matches 35; Conservative 22; Mismatches 51; Indels 19; Gaps 7;

QY 8 ARSEGASALASVPLKTVTEALSRGWSVKSGETEDATKKKPLGVADANKL-----GT 63
DB 35 ARTQYTRAVSEVSAKTAESAILEGKEIVS-----SATPKDTQYDIGTETESTLDDGSK 89
QY 64 IALK-PDPAAGTADITLFTFMG-GAGPKNKKIITLRTADGLMKCTSDQ-----DEOF 116
DB 90 SOIQVTBQDQGT--VELVATLTKSSGSAIKGAVITVSR-KNDGVNCKITKTPAMKPY 146
QY 117 IPKCSR 123
DB 147 APANCPK 153

RESULT 9

US-07-638-492-2
Sequence 2, Application US/07638492
Patent No. 5494672
GENERAL INFORMATION:
APPLICANT: Hodges, Robert S.
APPLICANT: Paranchych, William
APPLICANT: Irvin, Randall T.
APPLICANT: Lee, Kok K.
APPLICANT: Parimi, Sastry A.
APPLICANT: Zoutman, Dick E.
APPLICANT: Dohy, Peter C.
APPLICANT: Wong, Mah Y.
TITLE OF INVENTION: Pseudomonas Peptide Composition and
TITLE OF INVENTION: Method
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/638,492
FILING DATE: 04-JAN-1991
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8900-0002.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: peptide 2
US-07-638-492-2

Query Match 15.2%; Score 96; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.1e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 KCTSDQDEQIFPKCSR 123
DB 1 KCTSDQDEQIFPKCSR 17

RESULT 10

US-08-084-739-5
Sequence 5, Application US/08084739
Patent No. 5468484
GENERAL INFORMATION:
APPLICANT: Hodges, Robert S.
APPLICANT: Irvin, Randall T.
APPLICANT: Paranchych, William
APPLICANT: Sokol, Pamela A.
APPLICANT: Woods, Donald E.
TITLE OF INVENTION: Pseudomonas Exoenzyme S Peptide
TITLE OF INVENTION: Composition and Method
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/084,739
FILING DATE: 28-JUN-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/721,759
FILING DATE: 25-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8900-0004.30
TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: both
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: PAK, Fig. 8
US-08-084-739-5

Query Match 14.7%; Score 93; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 7e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 107 KCTSDDEOFIPKCSR 123
DB 1 KCTSDDEOFIPKCSR 17

RESULT 11
US-07-638-492-1
Sequence 1, Application US/07638492
Patent No. 5494672
GENERAL INFORMATION:
APPLICANT: Hodges, Robert S.
APPLICANT: Paranchych, William
APPLICANT: Irvin, Randall T.
APPLICANT: Lee, Kok K.
APPLICANT: Parimi, Sastri A.
APPLICANT: Zouman, Dick E.
APPLICANT: Wong, Peter C.
APPLICANT: Wong, Wah Y.
TITLE OF INVENTION: Pseudomonas Peptide Composition and
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESS: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/638,492
FILING DATE: 04-JAN-1991
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Shultz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8900-0002.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: peptide 1

US-07-638-492-1

Query Match 14.7%; Score 93; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 7e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 107 KCTSDDEOFIPKCSR 123
DB 1 KCTSDDEOFIPKCSR 17

RESULT 12
US-08-260-199A-1
Sequence 1, Application US/08260199A
Patent No. 5738996
GENERAL INFORMATION:
APPLICANT: Hodges, Robert S.
APPLICANT: Irvin, Randall T.
APPLICANT: Holm, A.
APPLICANT: Wong, W.Y.
APPLICANT: Sheth, H.B.
APPLICANT: Husband, Devon L.
TITLE OF INVENTION: Combinatorial Library Composition and
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESS: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/260,199A
FILING DATE: 15-JUN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dehlinger, Peter J.
REGISTRATION NUMBER: 28,006
REFERENCE/DOCKET NUMBER: 8900-0008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Pseudomonas aeruginosa strain K
US-08-260-199A-1

Query Match 14.7%; Score 93; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 7e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 107 KCTSDDEOFIPKCSR 123
DB 1 KCTSDDEOFIPKCSR 17

RESULT 13
5445818-10
; Patent No. 5445818
; APPLICANT: HODGES, ROBERT S.; PARANCHYCH, WILLIAM; LEE, KOK K.;
; PARIMI, SASTRY A.; IRVIN, RANDALL T.; DOIG, PETER C.
; TITLE OF INVENTION: SYNTHETIC PSEUDOMONAS AERUGINOSA PILIN
; PEPTIDE VACCINE AND METHOD OF USE
; NUMBER OF SEQUENCES: 10
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/927,797
; FILING DATE: 10-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 344,565
; FILING DATE: 28-APR-1989
; SEQ ID NO:10:
; LENGTH: 16
5445818-10

Query Match 14.4%; Score 91; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 KCTSDDEQFIPKGS 122
Db 1 KCTSDDEQFIPKGS 16

RESULT 14
US-08-194-290-8
; Sequence 8, Application US/08194290
; Patent No. 5500353
; GENERAL INFORMATION:
; APPLICANT: Smit, John
; APPLICANT: Bingle, Wade H
; TITLE OF INVENTION: Bacterial surface protein expression
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Shlesinger, Arkwright & Garvey
; STREET: 3000 South Eads Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/194,290
; FILING DATE: 09-FEB-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Garvey, George A
; REGISTRATION NUMBER: 17737
; REFERENCE/DOCKET NUMBER: 5946-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-684-5600
; TELEFAX: 703-836-5288
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-194-290-8

Query Match 13.6%; Score 86; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.00047;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 CTSDDDEQFIPKGS 122
Db 2 CTSDDDEQFIPKGS 16

RESULT 15
US-08-614-377A-8
; Sequence 8, Application US/08614377A
; Patent No. 5976864
; GENERAL INFORMATION:
; APPLICANT: Smit, John
; APPLICANT: Bingle, Wade H
; APPLICANT: No. 5976864ellini, John F.
; TITLE OF INVENTION: EXPRESSION AND SECRETION OF
; TITLE OF INVENTION: HETEROLOGOUS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson PC
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/614,377A
FILING DATE: 12-MAR-1996
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/194,290
FILING DATE: 09-FEB-1994
CLASSIFICATION: 435
APPLICATION NUMBER: US 07/895,367
FILING DATE: 09-JUNE-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Tsao, Y. Rocky
REGISTRATION NUMBER: 34053
REFERENCE/DOCKET NUMBER: 08106/002001.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-614-377A-8

Query Match 13.6%; Score 86; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.00047;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 CTSDDDEQFIPKGS 122
Db 2 CTSDDDEQFIPKGS 16

Search completed: February 8, 2002, 15:25:10
Job time: 115 sec

Fri Feb 8 15:44:50 2002

us-09-865-159-4.ral

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 8, 2002, 15:23:15 ; Search time 353.09 Seconds

(Without alignments)
96.723 Million cell updates/sec

Title: US-09-865-159-4

Perfect score: 631

Sequence: 1 ALEGEFARSEGASALASV.....GLMKCTSDDEQFIRKCSR 123

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 3148936 seqs, 277657034 residues

Total number of hits satisfying chosen parameters: 3148936

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Database :

Pending Patents AA Main: *
1: /cgn2_6/ptodata/2/paa/PCRNUS.COMB.pep.*
2: /cgn2_6/ptodata/2/paa/US06.COMB.pep.*
3: /cgn2_6/ptodata/2/paa/US07.COMB.pep.*
4: /cgn2_6/ptodata/2/paa/US08.COMB.pep.*
5: /cgn2_6/ptodata/2/paa/US081.COMB.pep.*
6: /cgn2_6/ptodata/2/paa/US082.COMB.pep.*
7: /cgn2_6/ptodata/2/paa/US083.COMB.pep.*
8: /cgn2_6/ptodata/2/paa/US084.COMB.pep.*
9: /cgn2_6/ptodata/2/paa/US085.COMB.pep.*
10: /cgn2_6/ptodata/2/paa/US086.COMB.pep.*
11: /cgn2_6/ptodata/2/paa/US087.COMB.pep.*
12: /cgn2_6/ptodata/2/paa/US088.COMB.pep.*
13: /cgn2_6/ptodata/2/paa/US089.COMB.pep.*
14: /cgn2_6/ptodata/2/paa/US090.COMB.pep.*
15: /cgn2_6/ptodata/2/paa/US091.COMB.pep.*
16: /cgn2_6/ptodata/2/paa/US092.COMB.pep.*
17: /cgn2_6/ptodata/2/paa/US093.COMB.pep.*
18: /cgn2_6/ptodata/2/paa/US094.COMB.pep.*
19: /cgn2_6/ptodata/2/paa/US095.COMB.pep.*
20: /cgn2_6/ptodata/2/paa/US096.COMB.pep.*
21: /cgn2_6/ptodata/2/paa/US097.COMB.pep.*
22: /cgn2_6/ptodata/2/paa/US098.COMB.pep.*
23: /cgn2_6/ptodata/2/paa/US099.COMB.pep.*
24: /cgn2_6/ptodata/2/paa/US60.COMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	631	100.0	123	17	US-09-329-884-4
2	612.5	97.1	169	17	US-09-329-884-14
3	611	96.8	169	17	US-09-329-884-12
4	325.5	51.6	122	17	US-09-329-884-6
5	307	48.7	168	17	US-09-329-884-22
6	305.5	48.4	168	17	US-09-329-884-20
7	147	23.1	129	17	US-09-329-884-10
8	146	23.1	129	17	US-09-329-884-2
9	134	21.2	127	17	US-09-329-884-8

	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	
	130	127.5	126	125.5	121	116	106.5	99.5	99.5	99.5	99.5	99.5	99.5	99.5	99.5	99.5	99.5	99.5	99.5	99.5	99.5	99.5	99.5	99.5	99.5	94	93	93	93	93	93	93	93	93	93	87	
	20.6	20.2	20.0	19.9	19.2	18.4	16.9	15.6	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	14.9	14.7	14.7	14.7	14.7	14.7	14.7	14.7	14.7	14.7	13.8	
	139	175	175	169	53	53	53	153	153	153	153	154	154	154	154	154	154	154	154	154	154	154	154	154	154	154	73	17	17	17	17	17	17	17	17	17	17
	US-09-848-616-140	US-09-329-884-18	US-09-329-884-16	US-09-328-352-6277	US-07-809-762A-27	US-09-252-991A-26702	US-07-809-762A-9	US-09-540-236-3689	US-60-128-476-4920	US-08-360-107-118	US-08-470-896-108	US-08-471-913-108	US-08-474-349-108	US-08-474-349A-108	US-08-475-668-108	US-08-484-223-108	US-08-484-223A-108	US-08-485-546-108	US-08-485-546A-108	US-08-485-551-108	US-08-487-266-108	US-08-487-266A-108	US-08-487-355-108	US-08-487-355A-108	US-08-919-600-108	US-09-502-445-108	US-08-540-397-14	PCT-US95-07764-1	PCT-US96-16032-5	US-08-245-507-18	US-08-540-397-16	US-09-306-241-1	US-09-345-624-1	US-09-345-624A-1	US-09-306-241-7	US-09-306-241-8	

ALIGNMENTS

RESULT 1
US-09-329-884-4
Sequence 4, Application US/09329884
GENERAL INFORMATION:
APPLICANT: Irvin, Randall T.
TITLE OF INVENTION: PSEUDOMONAS TREATMENT
FILE REFERENCE: 8900-0008.30
CURRENT FILING DATE: 1999-06-11
EARLIER APPLICATION NUMBER: US 60/089,155
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 123
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-329-884-4

Query Match 100.0%; Score 631; DB 17; Length 123;
Best Local Similarity 100.0%; Pred. No. 5.4e-64;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALEGEFARSEGASALASVNPILKTVEALISGWSVSGTGTEDATKKEVPLGVADANK 60
DB 1 ALEGEFARSEGASALASVNPILKTVEALISGWSVSGTGTEDATKKEVPLGVADANK 60
QY 61 LFTILKDDPPADGTADITLFTMGAGAPKKNKITTLETTADGLMKCTSDDEQFIRK 120

us-09-865-159-4.ram

Page 2

Query Match	48.7%;	Score 307;	DB 17;	Length 168;
Best Local Similarity	57.9%;	Pred. No. 1.4e-26;		
Matches	73;	Conservative	11;	Mismatches 32;
			Indels	10;
			Gaps	5

```

0Y 1 ALE---GGEPRRREGASALASVNPDKTTVEEALSRGMS---VKSCTGEDATKKEPVLG 54
Db 44 ALEKGGGGEPRRREGASALATINPLKTTVEESLSRGIAKSIKIGTAASTT--ETIYAV 101
0Y 55 AADANKLTIALKPPDADGTADITLTTLFTMGAGGGRNKKGIITLTLRTAAGLGIMKCTSPDDE 114
Db 102 EPDANKLTGIVIAVAIEDS-GAGDITFTTQTGTSSPKMATKTYITLTKRT-ADGWACKSTQDP 159
0Y 115 QFIPIRG 120
Db 160 MFTPIRG 165

```

```

RESULT      6
US-09-329-884-20
: Sequence 20, Application US/09329884
: GENERAL INFORMATION:
: APPLICANT:  Hodges, Randall T.
: TITLE OF INVENTION:  PSEUDOMONAS TREATMENT
: FILE REFERENCE:  8900-0008.30
: CURRENT APPLICATION NUMBER:  US/09/329,884
: CURRENT FILING DATE:  1999-06-11
: EARLIER APPLICATION NUMBER:  US 60/089,155
: EARLIER FILING DATE:  1998-06-12
: NUMBER OF SEQ ID NOS:  22
: SOFTWARE:  FastSeq for Windows Version 3.0
: SEQ ID NO 20
: LENGTH: 168
: TYPE:  PRT
: ORGANISM:  Pseudomonas aeruginosa
US-09-329-884-20

```

Query Match	48.4%	Score 305.5;	DB 17;	Length 168;
Best Local Similarity	58.3%;	Pred. M.2.le-26;		
Matches 70; Conservative	11;	Mismatches 32;	Indels 7;	Gaps 4.

Oy	4	GTEPRSGASLAVNPILKTTVEEALSRGMS---	VKSGTGEDATKKRVPGLVADANK	60
		:		
Db	50	GGEFARSGASLATINPLKTTVEESLRGIGSKIKITGTASTAT--	TTYAGVEPDANK	107
		:		
Oy	61	LGTIILKDDPADAGTDTLTFTMGAGPNKKKIITLLFTTAADGLMKCSDDEOEIFPKK		120
		: :		
Db	108	LGVIAVAIEDS--GADDITFTTFOTGISPFNNAKRVITIANT--	ADGWACACSTODPMATTTPKG	165
		:		

```

1  RESULT: 7
2  US-09-329-884-10
3  : Sequence 10, Application US/09329884
4  : GENERAL INFORMATION:
5  :
6  : APPLICANT: Irvlin, Randall T.
7  :
8  : TITLE OF INVENTION: PSEUDOMONAS TREATMENT
9  : TITLE OF INVENTION: COMPOSITION AND METHO
10 : FILE REFERENCE: 8900-0008, 30
11 :
12 : CURRENT APPLICATION NUMBER: US/09/329,884
13 :
14 : CURRENT FILING DATE: 1999-06-11
15 :
16 : EARLIER APPLICATION NUMBER: US 60/089,155
17 :
18 : EARLIER FILING DATE: 1998-06-12
19 :
20 : NUMBER OF SEQ ID NOS: 22
21 :
22 : SOFTWARE: PASTSDQ for Windows Version 3.0
23 :
24 : SEQ ID NO 10
25 :
26 : LENGTH: 127
27 :
28 : TYPE: PRT
29 :
30 : ORGANISM: Pseudomonas aeruginosa
31 :
32 : US-09-329-884-10

```

Query Match	23.3%;	Score 147;	DB 17;	Length 127;
Best Local Similarity	33.8%;	Pred. No. 2.2e-08;		
Matches 44;	Conservative 16;	Mismatches 58;	Indels 12;	Gaps 5

```

0Y 1 ALEGEPFRSRGASLASVNPFLKTTVEEALSRGMSVSGTGT-----EATKKEVPLGV 54
   | | | | | | | | : : | | | | | | | | : : | |
Db 1 ALEGIEFRSROVSRVMAPAGSLKTAVEACLDDG---RTAVGTAAGQCDPGATGSSLLTGA 57
   | | | | | | | | : : | | | | | | | | : : | |
QY 55 AADANKLCTIATLKPPDADG-TADITLTFYTMG-GAGPRNKGIITLPTAADGLMKCTSDQ 112
   : : : | | | | | | | | : : | | | | | | : : | |
Db 58 SQTSGTLETPNGVQVLDPLTQTITATPBNGBASAI SGTLTWTRD-VNGGMSCATIV 116
   : : : | | | | | | | | : : | | | | | | : : | |
QY 113 DEQFIKPGKS 122
   | : | | | | | | : : | | | | | | : : | |
Db 117 DAKFRPNCGT 126

```

```

RESULT      8
US-09-329-884-2
: Sequence 2, Application US/09329884
: GENERAL INFORMATION:
: APPLICANT: Ilyin, Randall T.
: APPLICANT: Hodges, Robert S.
: TITLE OF INVENTION: PSEUDOMONAS TREATMENT
: TITLE OF INVENTION: COMPOSITION AND METHOD
: FILE REFERENCE: 8900-0008.30
: CURRENT APPLICATION NUMBER: US/09/329,884
: CURRENT FILING DATE: 1999-06-11
: EARLIER APPLICATION NUMBER: US 60/089,155
: EARLIER FILING DATE: 1998-06-12
: NUMBER OF SEO ID NOS: 22
: SOFTWARE: FastSEO for Windows Version 3.0
: SEO ID NO 2
: LENGTH: 129
: TYPE: PRT
: ORGANISM: Pseudomonas aeruginosa
US-09-329-884-2

```

```

! Query Match Similarity      23.1%; Score 146; DB 17; Length 129;
! Best Local Similarity      31.7%; Pred No. 3e-08;
Matches      40; Conservative 17; Mismatches 59; Indels 10; Gaps 3

Qy      1 ALEGTGFARSEASALASVNPDKTYVEALSLGWSVSKCTGEDATKKEVPLG--VAADA 58
        |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      1 ALEGTGFARAAQLSEKRTILASGLKTKVSDLFSDGSCSPATTAATAGIEKPTDINGKYAVY 60

Qy      59 NKLGTALAKPDADPADTADITTLFTMGAGAPKNNKGIITLRTAADG--LWKCTSDODEQ 115
        |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      61 TTGGTAA-----ASGCGCTVATMKASDVATPLRGLKTLFTLGNADGKSTWACTSNADNK 115

Qy      116 FLPKGC 121
Db      116 YLPKTC 121

```

9
 US-09-329-884-8
 : Sequence 8, Application US/09329884
 : GENERAL INFORMATION:
 : APPLICANT: Irvlin, Randall T.
 : APPLICANT: Hodges, Robert S.
 : TITLE OF INVENTION: PSEUDOMONAS TREATMENT
 : TITLE OF INVENTION: COMPOSITION AND METHOD
 : FILE REFERENCE: 8900-0008, 30
 : CURRENT APPLICATION NUMBER: US/09/329, 884
 : CURRENT FILING DATE: 1999-06-11
 : EARLIER APPLICATION NUMBER: US 60/089, 155
 : EARLIER FILING DATE: 1998-06-12
 : NUMBER OF SEQ ID NOS: 22
 : SOFTWARE: FastSeq for Windows Version 3.0
 : SEQ ID NO 8
 : LENGTH: 127
 : TYPE: PRT
 : ORGANISM: Pseudomonas aeruginosa
 : US-09-329-884-8

Query Match 21.28; Score 134; DB 17; Length 127;
 Best Local Similarity 35.18; Pred. No. 6.9e-07;
 Matches 40; Conservative 19; Mismatches 41; Indels 14; Gaps 6;

OY 1 ALEGEFARSGASALASVNPDKTVEALSRGWSKSGTGTEDATKEVPLGVAADANK 60
 DB 1 ALEGEFARQVTRAVSEVSAKTAESALLESKEIVS-----SAPKDTQYDGFTEST 55
 OY 61 L-----GTIALK-PPADGTADITLFTTMG-GAGPKNKGIITLTPAADGKMC 108
 DB 56 LLDGSGSQIQVTDNKGDT--VELVATLKGSSGSAIKGAVIIVSR-KNDGVNMC 106

RESULT 10
 US-09-848-616-140
 ; Sequence 140, Application US/09848616
 ; GENERAL INFORMATION:
 ; APPLICANT: Seibel, Peter
 ; APPLICANT: Dunant, Nicolas
 ; APPLICANT: Bachmann, Martin
 ; APPLICANT: Tissot, Alain
 ; APPLICANT: Lechner, Franziska
 ; TITLE OF INVENTION: Molecular Antigen Array
 ; FILE REFERENCE: 1700.0180002
 ; CURRENT APPLICATION NUMBER: US/09/848, 616
 ; CURRENT FILING DATE: 2001-05-05
 ; NUMBER OF SEQ ID NOS: 186
 ; SOFTWARE: Patentln Ver. 2.1
 ; SEQ ID NO 140
 ; LENGTH: 139
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas stutzeri
 ; US-09-848-616-140

Query Match 20.68; Score 130; DB 22; Length 139;
 Best Local Similarity 36.48; Pred. No. 2.3e-06;
 Matches 44; Conservative 10; Mismatches 41; Indels 26; Gaps 6;

OY 9 RSEBASALASVNPDKTVEALSRG-----WSYKSG-TGTEDATK-EPPLVADANKL 61
 DB 38 RSNAAALAITPGKIGFEQAINEGKTPSLTSDGYITITSTICDDVLDLTADGH-- 95
 OY 62 GTIALKPPADGTADITLFTTMGAGPKNKGIITLTPAADGLKCTSDODEPIPKGC 121
 DB 96 -----TECTAKGSGMG-KPDGKTTILNRT-ADGEMSCASTLDATKYKPGKC 138
 OY 122 S 122
 DB 139 S 139

RESULT 11
 US-09-329-884-18
 ; Sequence 18, Application US/09329884
 ; GENERAL INFORMATION:
 ; APPLICANT: Irvin, Randall T.
 ; APPLICANT: Hodges, Robert S.
 ; TITLE OF INVENTION: PSEUDOMONAS TREATMENT
 ; FILE REFERENCE: 8900-0008.30
 ; CURRENT APPLICATION NUMBER: US/09/329, 884
 ; CURRENT FILING DATE: 1999-06-11
 ; EARLIER APPLICATION NUMBER: US 60/089,155
 ; EARLIER FILING DATE: 1998-06-12
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 18
 ; LENGTH: 175
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa

US-09-329-884-18

Query Match 20.28; Score 127.5; DB 17; Length 175;
 Best Local Similarity 30.28; Pred. No. 6.1e-06;
 Matches 39; Conservative 17; Mismatches 60; Indels 13; Gaps 4;

OY 1 ALE-----GTEFARSGASALASVNPDKTVEALSRGWSKSGTGTEDATKEVPLG--VA 55
 DB 44 ALEGGGGEFARQLESMRTIASGLTKVSDIFSDGSCPANTATAGIEKDDINGKYV 103
 OY 56 ADANKGTIALKPPADGTADITLFTTMGAGPKNKGIITLTPAADG---LWKCTSDQ 112
 DB 104 AKVTTGTA-----ASGCTIVATMKASDVATPLRGKTTTLTLGNADKSGTYWACTSMA 158
 OY 113 DEQPIPKGC 121
 DB 159 DNKYLKTC 167

RESULT 12
 US-09-329-884-16
 ; Sequence 16, Application US/09329884
 ; GENERAL INFORMATION:
 ; APPLICANT: Irvin, Randall T.
 ; APPLICANT: Hodges, Robert S.
 ; TITLE OF INVENTION: PSEUDOMONAS TREATMENT
 ; FILE REFERENCE: 8900-0008.30
 ; CURRENT APPLICATION NUMBER: US/09/329, 884
 ; CURRENT FILING DATE: 1999-06-11
 ; EARLIER APPLICATION NUMBER: US 60/089,155
 ; EARLIER FILING DATE: 1998-06-12
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 16
 ; LENGTH: 175
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 ; US-09-329-884-16

Query Match 20.08; Score 126; DB 17; Length 175;
 Best Local Similarity 29.38; Pred. No. 9.1e-06;
 Matches 36; Conservative 17; Mismatches 60; Indels 10; Gaps 3;

OY 4 GTEFARSGASALASVNPDKTVEALSRGWSKSGTGTEDATKEVPLG--VAADANKL 61
 DB 50 GGEFARQLESMRTIASGLTKVSDIFSDGSCPANTATAGIEKDDINGKYVAKVTTG 109
 OY 62 GTIALKPPADGTADITLFTTMGAGPKNKGIITLTPAADG---LWKCTSDODEPIPK 118
 DB 110 GTAA-----ASGCTIVATMKASDVATPLRGKTTTLTLGNADKSGTYWACTSMA 164
 OY 119 KGC 121
 DB 165 KTC 167

RESULT 13
 US-09-328-352-6277
 ; Sequence 6277, Application US/09328352
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary L. Breton et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACT.
 ; FILE REFERENCE: GTC99-03PA
 ; CURRENT APPLICATION NUMBER: US/09/328,352
 ; CURRENT FILING DATE: 1999-06-04
 ; NUMBER OF SEQ ID NOS: 8252
 ; SEQ ID NO 6277
 ; LENGTH: 169
 ; TYPE: PRT

Fri Feb 8 15:44:50 2002

us-09-865-159-4.rpm

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 8, 2002, 15:23:15 ; Search time 37.1 Seconds

(without alignments)
147.610 Million cell updates/sec

Title: US-09-865-159-4

Perfect score: 631
Sequence: 1 ALEGTFFARSEGASALASVN.....GLMKCHSDDEQFIPKCSR 123

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 211743 seqs, 44522877 residues

Total number of hits satisfying chosen parameters: 211743

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Pending_Patents_AA_New:*
1: /cgn2_6/ptodata/2/paa/PCN_NEW_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	631	100.0	123	5	US-09-865-159-4
2	612.5	97.1	169	5	US-09-865-159-14
3	611	96.8	169	5	US-09-865-159-12
4	325.5	51.6	122	5	US-09-865-159-6
5	307	48.7	168	5	US-09-865-159-22
6	305.5	48.4	168	5	US-09-865-159-20
7	147	23.3	127	5	US-09-865-159-10
8	146	23.1	129	5	US-09-865-159-2
9	134	21.2	127	5	US-09-865-159-8
10	127.5	20.2	175	5	US-09-865-159-18
11	126	20.0	175	5	US-09-865-159-16
12	82.5	13.1	183	5	US-09-675-784A-12256
13	74	11.7	585	5	US-09-605-703B-1960
14	73.5	11.6	231	6	US-10-029-120-18
15	73.5	11.6	231	6	US-10-027-806-18
16	73.5	11.6	231	6	US-10-034-623-18
17	73.5	11.6	480	5	US-09-897-516-8177
18	73.5	11.6	1531	5	US-09-995-493-44
19	73	11.6	461	5	US-09-708-427-53349
20	73	11.6	488	5	US-09-708-427-53348
21	72.5	11.5	649	5	US-09-708-427-34069
22	72	11.4	215	5	US-09-620-394B-5236
23	72	11.4	236	5	US-09-620-394B-5235
24	72	11.4	298	5	US-09-620-394B-5234
25	72	11.4	639	5	US-09-571-553A-18
26	72	11.4	639	5	US-09-571-553A-19

27	72	11.4	639	5	US-09-571-553A-20	Sequence 20, Appl
28	72	11.4	639	5	US-09-571-553A-21	Sequence 21, Appl
29	71.5	11.3	178	6	US-10-029-386-33528	Sequence 33528, A
30	71.5	11.3	334	5	US-09-708-427-63649	Sequence 63649, A
31	69.5	11.0	429	5	US-09-806-866-71	Sequence 71, Appl
32	68	10.8	183	5	US-09-620-394B-5850	Sequence 5850, Ap
33	68	10.8	187	5	US-09-620-394B-5849	Sequence 5849, Ap
34	68	10.8	200	5	US-09-620-394B-5848	Sequence 5848, Ap
35	68	10.8	304	5	US-09-708-427-34740	Sequence 34740, A
36	68	10.8	312	5	US-09-708-427-34739	Sequence 34739, A
37	68	10.8	454	5	US-09-708-427-34738	Sequence 34738, A
38	68	10.8	576	5	US-09-708-427-11330	Sequence 11330, A
39	68	10.8	586	5	US-09-708-427-11329	Sequence 11329, A
40	68	10.8	639	5	US-09-571-553A-10	Sequence 10, Appl
41	68	10.8	639	5	US-09-571-553A-11	Sequence 11, Appl
42	68	10.8	639	5	US-09-571-553A-12	Sequence 12, Appl
43	68	10.8	639	5	US-09-571-553A-13	Sequence 13, Appl
44	68	10.8	639	5	US-09-571-553A-14	Sequence 14, Appl
45	68	10.8	639	5	US-09-571-553A-15	Sequence 15, Appl

ALIGNMENTS

```
RESULT 1
US-09-865-159-4
Sequence 4, Application US/09865159
GENERAL INFORMATION:
APPLICANT: Irvin, Randall T.
TITLE OF INVENTION: PSEUDOMONAS TREATMENT
TITLE OF INVENTION: COMPOSITION AND METHOD
FILE REFERENCE: 8900-0008.30
CURRENT APPLICATION NUMBER: US/09/865.159
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329,884
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 123
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-865-159-4

Query Match      100.0%; Score 631; DB 5; Length 123;
Best Local Similarity 100.0%; Pred. No. 2.3e-60;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ALEGTFFARSEGASALASVNPDKTVEEALSRGWSKSGTGTEDATKKEVPLGVAADANK 60
      |||||||
DB      1 ALEGTFFARSEGASALASVNPDKTVEEALSRGWSKSGTGTEDATKKEVPLGVAADANK 60

QY      61 LGTALKRPDAGTADITLFTFMGAGPKNKGIITLRTADGLMKCHSDDEQFIPKG 120
      |||||||
DB      61 LGTALKRPDAGTADITLFTFMGAGPKNKGIITLRTADGLMKCHSDDEQFIPKG 120

QY      121 CSR 123
      |||
DB      121 CSR 123

RESULT 2
US-09-865-159-14
Sequence 14, Application US/09865159
GENERAL INFORMATION:
APPLICANT: Irvin, Randall T.
TITLE OF INVENTION: PSEUDOMONAS TREATMENT
TITLE OF INVENTION: COMPOSITION AND METHOD
FILE REFERENCE: 8900-0008.30
CURRENT APPLICATION NUMBER: US/09/865.159
```

```

; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329,884
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 169
; TYPE: PRF
; ORGANISM: Pseudomonas aeruginosa
US-09-865-159-14

```

```

Query Match          97.1%; Score 612.5; DB 5; Length 169;
Best Local Similarity 96.8%; Pred. No. 3,3e-58;
Matches 122; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

```

```

QY 1 ALE---GTEFARSEGASALASVNPDKTTVEEALSRGWSVSGTGEDATKKEVPLGVAAD 57
    ||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 44 ALEKGGGGEFARSEGASALASVNPDKTTVEEALSRGWSVSGTGEDATKKEVPLGVAAD 103
QY 58 ANKIGTIALKPPADGTADITLFTFMGAGAPKKNKGIITLRTAADGLMKCTSDODEQFI 117
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 104 ANKIGTIALKPPADGTADITLFTFMGAGAPKKNKGIITLRTAADGLMKCTSDODEQFI 163
QY 118 PKGCSR 123
    |||||
DB 164 PKGCSR 169

```

```

RESULT 3
US-09-865-159-12
; Sequence 12, Application US/09865159
; GENERAL INFORMATION:
; APPLICANT: Irvn, Randall T.
; APPLICANT: Hodges, Robert S.
; TITLE OF INVENTION: PSEUDOMONAS TREATMENT
; FILE REFERENCE: 8900-0008.30
; CURRENT APPLICATION NUMBER: US/09/865,159
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329,884
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 169
; TYPE: PRF
; ORGANISM: Pseudomonas aeruginosa
US-09-865-159-12

```

```

Query Match          96.8%; Score 611; DB 5; Length 169;
Best Local Similarity 99.2%; Pred. No. 4.8e-58;
Matches 119; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 4 GTEFARSEGASALASVNPDKTTVEEALSRGWSVSGTGEDATKKEVPLGVAADANKLGT 63
    ||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 50 GGEFARSEGASALASVNPDKTTVEEALSRGWSVSGTGEDATKKEVPLGVAADANKLGT 109
QY 64 IALKPPADGTADITLFTFMGAGAPKKNKGIITLRTAADGLMKCTSDODEQFI PKGCSR 123
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 110 IALKPPADGTADITLFTFMGAGAPKKNKGIITLRTAADGLMKCTSDODEQFI PKGCSR 169

```

```

RESULT 4
US-09-865-159-6
; Sequence 6, Application US/09865159
; GENERAL INFORMATION:
; APPLICANT: Irvn, Randall T.
; APPLICANT: Hodges, Robert S.
; TITLE OF INVENTION: PSEUDOMONAS TREATMENT
; FILE REFERENCE: 8900-0008.30

```

```

; CURRENT APPLICATION NUMBER: US/09/865,159
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329,884
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 122
; TYPE: PRF
; ORGANISM: Pseudomonas aeruginosa
US-09-865-159-6

```

```

Query Match          51.6%; Score 325.5; DB 5; Length 122;
Best Local Similarity 60.2%; Pred. No. 1.2e-27;
Matches 74; Conservative 11; Mismatches 31; Indels 7; Gaps 4;

```

```

QY 1 ALEGEFARSEGASALASVNPDKTTVEEALSRGWS---VKSCTGEDATKKEVPLGVAAD 57
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1 ALEGEFARSEGASALASVNPDKTTVEEALSRGWSKIKIGTASTAT--ETVAGVDP 58
QY 58 ANKIGTIALKPPADGTADITLFTFMGAGAPKKNKGIITLRTAADGLMKCTSDODEQFI 117
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 59 ANKIGTIALKPPADGTADITLFTFMGAGAPKKNKGIITLRTAADGLMKCTSDODEQFI 116
QY 118 PKG 120
    |||
DB 117 PKG 119

```

```

RESULT 5
US-09-865-159-22
; Sequence 22, Application US/09865159
; GENERAL INFORMATION:
; APPLICANT: Irvn, Randall T.
; APPLICANT: Hodges, Robert S.
; TITLE OF INVENTION: PSEUDOMONAS TREATMENT
; FILE REFERENCE: 8900-0008.30
; CURRENT APPLICATION NUMBER: US/09/865,159
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329,884
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 168
; TYPE: PRF
; ORGANISM: Pseudomonas aeruginosa
US-09-865-159-22

```

```

Query Match          48.7%; Score 307; DB 5; Length 168;
Best Local Similarity 57.9%; Pred. No. 1.7e-25;
Matches 73; Conservative 11; Mismatches 32; Indels 10; Gaps 5;

```

```

QY 1 ALE---GTEFARSEGASALASVNPDKTTVEEALSRGWS---VKSCTGEDATKKEVPLGV 54
    ||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 44 ALEKGGGGEFARSEGASALASVNPDKTTVEEALSRGWSKIKIGTASTAT--ETVAGV 101
QY 55 AADANKLGTIALKPPADGTADITLFTFMGAGAPKKNKGIITLRTAADGLMKCTSDODE 114
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 102 FPDANKLGVIAVIEDS--GAGDITFTFTGTSSPRNATKVTTLNRT--ADGVWACKSTODP 159
QY 115 OFIPKG 120
    |||||
DB 160 MFTPKG 165

```

```

RESULT 6
US-09-865-159-20
; Sequence 20, Application US/09865159
; GENERAL INFORMATION:

```


Query Match 11.7%; Score 74; DB 5; Length 585;

Best Local Similarity	27.5%;	Pred.	No. 7.1;
Matches	28;	Conservative	19;
		Mismatches	43;
		Indels	12;
		Gaps	4;

```

RESULT 14
US-10-029-120-18
: Sequence 18, Application US/10029120
: GENERAL INFORMATION:
: APPLICANT: Swanson, Ronald V.
: APPLICANT: Feldman, Robert A.
: TITLE OF INVENTION: NOCLETE ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
: FILE REFERENCE: DCOIP 002A
: CURRENT APPLICATION NUMBER: US/10/029.120
: PRIOR FILING DATE: 2001-12-21
: PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/408,020
: PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-29
: NUMBER OF SEQ ID NOS: 123
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 18
: LENGTH: 231
: TYPE: PRT
: ORGANISM: Cenarchaeum symbiosum
US-10-029-120-18

```

[illegible]

```

RESULT 15
US-10-027-806-18
: Sequence 18, Application US/10027806
: GENERAL INFORMATION:
: APPLICANT: Swanson, Ronald V.
: APPLICANT: Schleper, Christa
: TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
: FILE REFERENCE: DCOIP-002A
: CURRENT APPLICATION NUMBER: US/10/027,806
: CURRENT FILING DATE: 2001-12-21
: PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/408,020
: PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-29
: NUMBER OF SEQ ID NOS: 123
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 18
: LENGTH: 231
: TYPE: PRT
: ORGANISM: Cenarchaeum symbiosum
US-10-027-806-18

```

```

Query Match          11.6% Score 73.5; DB 6; Length 231;
Best Local Similarity 24.8%; Pred. No. 2.5;
Matches 30; Conservative 15; Mismatches 39; Indels 37; Gaps 5;

OY      2 LEGTEFARSEGASALASYNP LKTTVEEALSRGWSVKSQTG-----TEDATKKE 49
         || | | | | | | | | | | | | | | | | | | | | : : : |
Db       115 LEENHYAYASESGWCLD-----RHGETGFPPKTTGGAPEPYPRRLDSENVRRRE 165

OY      50 VPLGYAADANKIKGTALKRPDPADGTADITLFTTGG-----AGPKNGKIIT 96
         || | | | | | | | | | | | | | | | | | | | | : : : |
Db       166 IDTGVALE--KL-RVKLRGPEDPGMRDLREEFAVRSVVEEVAPYVESRLVGKKKRVIMR 222

OY      97 L 97
         |
Db       223 I 223

```

Search completed: February 8, 2002, 15:26:38
Job time: 203 sec

Fri Feb 8 15:44:51 2002

us-09-865-159-4.rpn

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 8, 2002, 15:24:31 ; Search time 67.74 Seconds

(without alignments)
133,406 Million cell updates/sec

Title: US-09-865-159-6

Perfect score: 612
Sequence: 1 ALEGEFARSEGASALATIN.....GWACKSTODPMFTKGSND 122

Scoring table: BLOSOM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_1101.*
1: /SIDS8/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SIDS8/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SIDS8/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SIDS8/gcgdata/geneseq/geneseq/AA1983.DAT.*
5: /SIDS8/gcgdata/geneseq/geneseq/AA1984.DAT.*
6: /SIDS8/gcgdata/geneseq/geneseq/AA1985.DAT.*
7: /SIDS8/gcgdata/geneseq/geneseq/AA1986.DAT.*
8: /SIDS8/gcgdata/geneseq/geneseq/AA1987.DAT.*
9: /SIDS8/gcgdata/geneseq/geneseq/AA1988.DAT.*
10: /SIDS8/gcgdata/geneseq/geneseq/AA1989.DAT.*
11: /SIDS8/gcgdata/geneseq/geneseq/AA1990.DAT.*
12: /SIDS8/gcgdata/geneseq/geneseq/AA1991.DAT.*
13: /SIDS8/gcgdata/geneseq/geneseq/AA1992.DAT.*
14: /SIDS8/gcgdata/geneseq/geneseq/AA1993.DAT.*
15: /SIDS8/gcgdata/geneseq/geneseq/AA1994.DAT.*
16: /SIDS8/gcgdata/geneseq/geneseq/AA1995.DAT.*
17: /SIDS8/gcgdata/geneseq/geneseq/AA1996.DAT.*
18: /SIDS8/gcgdata/geneseq/geneseq/AA1997.DAT.*
19: /SIDS8/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SIDS8/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SIDS8/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	612	100.0	122	AAV4377	Exemplary truncate
2	593.5	97.0	168	AAV4385	P.aeruginosa E coli
3	592	96.7	21	AAV4384	P.aeruginosa H co
4	325.5	53.2	21	AAV4376	Exemplary truncate
5	307	50.2	169	AAV4381	P.aeruginosa E coli
6	305.5	49.9	21	AAV4380	P.aeruginosa H co
7	137.5	22.5	127	AAV4378	Exemplary truncate
8	133.5	21.8	127	AAV4379	Exemplary truncate
9	109.5	17.9	21	AAV4375	Exemplary truncate
10	99.5	16.3	53	AAV4383	P.aeruginosa E coli
11	91	14.9	175	AAV4383	P.aeruginosa E coli

12	90	14.7	17	13	AAV25900	P.aeruginosa PAO pl
13	90	14.7	17	17	AAV86704	Pilin derived pept
14	90	14.7	17	21	AAV49351	P.aeruginosa PAO
15	90	14.7	17	21	AAV49351	Cell surface bindi
16	89.5	14.6	175	21	AAV44382	P.aeruginosa H co
17	84	13.7	595	21	AAV52370	Escherichia coli F
18	82.5	13.5	568	22	AAV49639	Escherichia coli H
19	80.5	13.2	498	22	AAV49641	Escherichia coli H
20	78.5	12.8	498	8	AAV70302	Sequence of flagel
21	76	12.4	413	14	AAV41547	Hsp150. Saccharom
22	75	12.3	14	11	AAV86813	Hsp150 (Heat Shock
23	75	12.3	14	21	AAV808101	PAO polypeptide de
24	75	12.3	14	21	AAV49359	C-terminal pilin p
25	75	12.3	653	22	AAV93085	Human protein sequ
26	75	12.3	1213	22	AAV40016	Human polypeptide
27	74.5	12.2	639	17	AAV00366	Streptomyces lacto
28	74	12.1	558	20	AAV00143	Enterococcus faeca
29	74	12.1	1638	20	AAV00138	Enterococcus faeca
30	74	12.1	1638	20	AAV00140	Enterococcus faeca
31	74	12.1	1638	20	AAV00142	Enterococcus faeca
32	73.5	12.0	1026	17	AAV7374	Phage T4 tail fibr
33	73.5	12.0	1026	20	AAV94678	Bacteriophage T4 t
34	73.5	12.0	1026	20	AAV92358	Bacteriophage T4 t
35	73.5	12.0	1026	22	AAV35154	Bacteriophage T4 g
36	72	11.8	274	17	AAV54529	Subtilisin Carlsbe
37	72	11.8	413	22	AAV30774	C glutaminc prote
38	72	11.8	441	22	AAV79050	Corynebacterium gl
39	71.5	11.7	268	20	AAV24909	Bacillus subtilis
40	71.5	11.7	619	22	AAV3993	Human protein sequ
41	71.5	11.7	2819	22	AAV35408	Human OTCG27 gene
42	70.5	11.5	264	18	AAV12716	Pha gene product.
43	70	11.4	659	18	AAV24123	Protease. Synthet
44	69.5	11.4	268	19	AAV62223	Subtilase BVSAB
45	69.5	11.4	268	20	AAV21647	Subtilase BVSAB.

ALIGNMENTS

RESULT 1
ID AAV4377 standard; Protein: 122 AA.
XX
AC AAV4377;
XX
DT 14-MAR-2000 (first entry)
XX
DE Exemplary truncated P. aeruginosa PAO pilin protein.
XX
KW Modified PAO pilin protein: alpha-helical forming portion;
KW Pseudomonas infection; cystic fibrosis; neutropenia.
XX
OS Pseudomonas aeruginosa.
XX
PN WO9965511-A2.
XX
PD 23-DEC-1999.
XX
PE 11-JUN-1999; 99WO-CA00554.
XX
PR 12-JUN-1998; 98US-0089155.
XX
PA (UYAL-) UNIV ALBERTA.
XX
PI Hodges RS, Irvin RT;
XX
DR WPI: 2000-106013/09.
XX
DR N-PSDB: AAV29536.
XX
PT Composition for treating or preventing Pseudomonas aeruginosa infection
XX
PS comprising pilin protein that can not self-assemble -
Claim 9; Fig 1C; 32pp; English.

XX The present sequence is the modified PAO pilin protein from
 CC P.aeruginosa. The N-terminal peptide region preferably lacks the first
 CC 15-40 residues of native P.aeruginosa. Modified pilin proteins are
 CC prepared by PCR amplification of pilin coding sequences using primers
 CC that effect the desired deletion, modification or insertion of a coiled-
 CC coil moiety in the coding sequences. The modified protein thus lacks a
 CC critical alpha-helical forming portion. This prevents oligomerisation of
 CC pilin protein necessary for attachment to the host cell during infection.
 CC The ligated plasmid DNA was transformed into an expression host. The
 CC modified pilin protein is useful in treatment and prophylaxis for
 CC individuals at risk of Pseudomonas infection, e.g. cystic fibrosis
 CC patients, burn patients, and severe neutropenic patients.

SO Sequence 122 AA:

Query Match 100.0%; Score 612; DB 21; Length 122;
 Best Local Similarity 100.0%; Pred. No. 1.1e-58;
 Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALEGEFARSEGASALATINPLKTTVEESLSRGISGKIKIGTASTATETTYAGVDPAN 60
 DB 1 alegetefarsegasalatlnplktveeslsrgisgskikigtastatetyagvdpdn 60
 QY 61 KLGVAVAVIEDSGAGDITFTFOTGTSSEKRNATKVITLNRADGVWACKSTODPMFTPKGS 120
 DB 61 klgyavaviedsgagdlftftqgtsspnatkvtltnradgywackstodpmtfpkgs 120
 QY 121 DN 122
 DB 121 dn 122

RESULT 2

AAV4385
 ID AAV4385 standard; Protein; 168 AA.

XX AAV4385;

DT 14-MAR-2000 (first entry)

DE P.aeruginosa E coil-truncated PAO pilin protein.

KW Modified PAO pilin protein; alpha-helical forming portion; E coil;
 KW Exemplary coil; coiled coil heterodimer; host cell-receptor site;
 OS Pseudomonas infection; cystic fibrosis; neutropenia.

OS Pseudomonas aeruginosa.

PN WO965511-A2.

PD 23-DEC-1999.

PF 11-JUN-1999; 99WO-CA00554.

PR 12-JUN-1998; 98US-0089155.

PA (UYAL-) UNIV ALBERTA.

PI Hodges RS, Irvin RT;

DR WPI: 2000-106013/09.

DR N-PSDB; AA229544.

PT Composition for treating or preventing Pseudomonas aeruginosa infection
 PT comprising pilin protein that can not self-assemble.

PS Claim 1; Fig 5B; 32pp; English.

CC The present sequence encodes E coil truncated PAO pilin protein from
 CC P.aeruginosa. The first 15-40 residues of the N-terminal peptide region
 CC is replaced by a peptide segment capable of forming a coiled-coil

CC heterodimer with an oppositely charged peptide segment which can form
 CC dimeric structures. These proteins are less inflammatory due to reduced
 CC degree of mobilisation of host-cell receptor sites. This prevents
 CC oligomerisation of pilin protein necessary for attachment to the host
 CC cell during infection. The modified pilin protein is useful in treatment
 CC e.g. cystic fibrosis patients, burn patients, and severe neutropenic
 CC patients.

SO Sequence 168 AA:

Query Match 97.0%; Score 593.5; DB 21; Length 168;
 Best Local Similarity 96.8%; Pred. No. 1.7e-56;
 Matches 121; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

QY 1 ALE--GTEFARSEGASALATINPLKTTVEESLSRGISGKIKIGTASTATETTYAGV 57
 DB 44 alekgygefeafarsegasalatlnplktveeslsrgisgskikigtastatetyagv 103
 QY 58 DANKIGVAVAVIEDSGAGDITFTFOTGTSSEKRNATKVITLNRADGVWACKSTODPMFT 117
 DB 104 danklgyavaviedsgagdlftftqgtsspnatkvtltnradgywackstodpmtfp 163
 QY 118 KGS DN 122
 DB 164 kgsdn 168

RESULT 3

AAV4384
 ID AAV4384 standard; Protein; 168 AA.

XX AAV4384;

DT 14-MAR-2000 (first entry)

DE P.aeruginosa H coil-truncated PAO pilin protein.

KW Modified PAO pilin protein; alpha-helical forming portion;
 KW coiled coil homodimer; host cell-receptor site; Pseudomonas infection;
 OS cystic fibrosis; neutropenia.

OS Pseudomonas aeruginosa.

PN WO965511-A2.

PD 23-DEC-1999.

PF 11-JUN-1999; 99WO-CA00554.

PR 12-JUN-1998; 98US-0089155.

PA (UYAL-) UNIV ALBERTA.

PI Hodges RS, Irvin RT;

DR WPI: 2000-106013/09.

DR N-PSDB; AA229543.

PT Composition for treating or preventing Pseudomonas aeruginosa infection
 PT comprising pilin protein that can not self-assemble.

PS Claim 1; Fig 5A; 32pp; English.

CC The present sequence is the H coil truncated PAO pilin protein from
 CC P.aeruginosa. The first 15-40 residues of the N-terminal peptide region
 CC is replaced by a peptide segment capable of forming a coiled-coil
 CC homodimer with an identical peptide segment which can form dimeric
 CC structures. These proteins are less inflammatory due to reduced degree of
 CC mobilisation of host-cell receptor sites. This prevents oligomerisation
 CC of pilin protein necessary for attachment to the host cell during
 CC infection. The modified pilin protein is useful in treatment and

QY 56 EPDANKLGIVAVAIEDS-GAGDITFTFQGTSSPKNATKVTILNRT-ADGVWACKSTODP 113
 Db 101 aadanklgitalkpdpadgadtltlftmgagpknkgtlilttrtaadglwksdsdqe 160
 QY 114 METPKG 119
 Db 161 qfipkg 166

RESULT 6

AAV44380
 ID AAV44380 standard; Protein; 169 AA.

AC AAV44380;

DT 14-MAR-2000 (first entry)

DE P. aeruginosa H coil-truncated PAK pilin protein.

XX Modified PAK pilin protein; alpha-helical forming portion;
 KW coiled coil homodimer; host cell-receptor site; Pseudomonas infection;
 XX cystic fibrosis; neutropenia.

OS Pseudomonas aeruginosa.

XX WO9965511-A2.

XX 23-DEC-1999.

XX 11-JUN-1999; 99WO-CA00554.

XX 12-JUN-1998; 98US-0089155.

XX (UVAL-) UNIV ALBERTA.

PI Hodges RS, Irvln RT;

DR WPI; 2000-106013/09.

DR N-PSDB; AAZ29539.

PT Composition for treating or preventing Pseudomonas aeruginosa infection

XX comprising pilin protein that can not self-assemble -

PS Claim 1; Fig 3A; 32pp; English.

XX The present sequence is the H coil truncated PAK pilin protein from
 CC P. aeruginosa. The first 15-40 residues of the N-terminal peptide region
 CC is replaced by a peptide segment capable of forming a coiled-coil
 CC homodimer with an identical peptide segment which can form dimeric
 CC structures. These proteins are less inflammatory due to reduced degree of
 CC mobilisation of host-cell receptor sites. This prevents oligomerisation
 CC of pilin protein necessary for attachment to the host cell during
 CC infection. The modified pilin protein is useful in treatment and
 CC prophylaxis for individuals at risk of Pseudomonas infection, and
 CC e.g. cystic fibrosis patients, burn patients, and severe neutropenic
 CC patients.

XX Sequence 169 AA;

Query Match 49.9%; Score 305.5; DB 21; Length 169;
 Best Local Similarity 58.3%; Pred. No. 2.6e-25;

Matches 70; Conservative 11; Mismatches 32; Indels 7; Gaps 4;

QY 4 GTEFARSEGASALATINPLKTTVEESLSRGAGSKIKIGTASTAT--ETVAGVDPDANK 61

Db 50 ggetarsegasalaalpklttveealsrgws--vksqgtedatkveplgvaadank 106

QY 62 LGVAVAIEDS-GAGDITFTFQGTSSPKNATKVTILNRT-ADGVWACKSTODPMETPKG 119

Db 107 lgtialkpdgadtltlftmgagpknkgtlilttrtaadglwksdsdqe qfipkg 166

RESULT 7

AAV44378
 ID AAV44378 standard; Protein; 127 AA.

AC AAV44378;

DT 14-MAR-2000 (first entry)

DE Exemplary truncated P. aeruginosa P1 pilin protein.

XX Modified P1 pilin protein; alpha-helical forming portion;
 KW Pseudomonas infection; cystic fibrosis; neutropenia.

OS Pseudomonas aeruginosa.

XX WO9965511-A2.

XX 23-DEC-1999.

XX 11-JUN-1999; 99WO-CA00554.

XX 12-JUN-1998; 98US-0089155.

XX (UVAL-) UNIV ALBERTA.

PI Hodges RS, Irvln RT;

DR WPI; 2000-106013/09.

DR N-PSDB; AAZ29537.

PT Composition for treating or preventing Pseudomonas aeruginosa infection

XX comprising pilin protein that can not self-assemble -

PS Claim 9; Fig 1D; 32pp; English.

XX The present sequence is the modified P1 pilin protein from
 CC P. aeruginosa. The N-terminal peptide region preferably lacks the first
 CC 15-40 residues of native P. aeruginosa. Modified pilin proteins are
 CC prepared by PCR amplification of pilin coding sequences using primers
 CC that effect the desired deletion, modification or insertion of a coiled-
 CC coil moiety in the coding sequences. The modified protein thus lacks a
 CC critical alpha-helical forming portion. This prevents oligomerisation of
 CC the ligated plasmid DNA for attachment to the host cell during infection.
 CC modified pilin protein is useful in treatment and prophylaxis for
 CC individuals at risk of Pseudomonas infection, e.g. cystic fibrosis
 CC patients, burn patients, and severe neutropenic patients.

XX Sequence 127 AA;

Query Match 22.5%; Score 137.5; DB 21; Length 127;
 Best Local Similarity 34.1%; Pred. No. 2.8e-07;

Matches 42; Conservative 18; Mismatches 42; Indels 21; Gaps 5;

QY 1 ALEGTFAESEGASALATINPLKTTVEESLSRG--TAGS-----KIKIGTASTATENVY 52

Db 1 alegtfartqytravseasalktaeasallegeksaelpktdyldgtfestsllid-- 58

QY 53 AGVEPDANKLGIVAVAIEDS-GAGDITFTFQGTSSPKNATK--VITLNRADGVWACKST 110

Db 59 -----gsqsgqgvcdnkdgvelvaltjgks--gsaikgavltvsirkndgwncklt 109

QY 111 QDP 113

Db 110 kcp 112

RESULT 8

AAV44379
 ID AAV44379 standard; Protein; 127 AA.

XX	AA44379;
DT	14-MAR-2000 (first entry)
DE	Exemplary truncated P. aeruginosa KB7 pilin protein.
XX	
KW	Modified KB7 pilin protein; alpha-helical forming portion;
KM	Pseudomonas infection; cystic fibrosis; neutropenia.
XX	
OS	Pseudomonas aeruginosa.
XX	
PN	WO965511-A2.
XX	
PD	23-DEC-1999.
XX	
PF	11-JUN-1999; 99WO-CA00554.
XX	
PR	12-JUN-1998; 98US-0089155.
XX	
PA	(UYAL-) UNIV ALBERTA.
PI	Hodges RS, Irvain RT;
DR	WPI: 2000-106013/09.
DR	N-PSDB: AA229538.
XX	
PT	Composition for treating or preventing Pseudomonas aeruginosa infection
XX	comprising pilin protein that can not self-assemble -
PS	
XX	Claim 9; Fig 1E; 32pp; English.
CC	The present sequence is the modified KB7 pilin protein from
CC	P. aeruginosa. The N-terminal peptide region preferably lacks the first
CC	15-40 residues of native P.aeruginosa. Modified pilin proteins are
CC	prepared by PCR amplification of pilin coding sequences using primers
CC	that effect the desired deletion, modification or insertion of a coiled-
CC	-coil moiety in the coding sequences. The modified protein thus lacks a
CC	critical alpha-helical forming portion. This prevents oligomerisation of
CC	pilin protein necessary for attachment to the host cell during infection.
CC	The ligated plasmid DNA was transformed into an expression host. The
CC	modified pilin protein is useful in treatment and prophylaxis for
CC	individuals at risk of Pseudomonas infection, e.g. cystic fibrosis
CC	patients, burn patients, and severe neutropenic patients.
XX	
SQ	Sequence 127 AA;
XX	
Query Match	21.8%; Score 133.5; DB 21; Length 127;
Best Local Similarity	31.8%; Pred. No. 7.5e-07;
Matches 41; Conservative 17; Mismatches 56; Indels 15; Gaps 4	
OY	1 ALEGTERRRSEGASLATTINPLKTTVESLSRGIAAGSKIKICTTA-----STATEVTAG 54 ::: : : : db 1 alegetfrrsgvsvrymaagslktaveaclqdg----rtavylaagqcpgatgsalllg 56 ::: : : :
OY	55 VEPDNNKL-----GVAVAVIEDSGADIFPFTGTSSPPNANKRVITINTADGWVACKST 110 57 asgtsgtclptntgyvpqvldipltqtllatigngasaaisg-qtlwtrdvngwscactl 115 ::: : : :
OY	111 QDPWFETPKG 119 ::: : : :
Dd	116 vdaKfrpng 124 ::: : : :
RESULT 9	
ID	AA44375
ID	AA44375 standard; Protein: 129 AA.
AC	AA44375;
XX	
DT	14-MAR-2000 (first entry)
XX	
XX	Exemplary truncated P. aeruginosa K122 pilin protein.

KX		Modified K122 pilin protein; alpha-helical forming portion;
KW		Pseudomonas infection; cystic fibrosis; neutropenia.
OS		Pseudomonas aeruginosa.
XX		
XX		MO965511-A2.
XX		
PD	23-DEC-1999.	
PF	11-JUN-1999;	99WO-CA00554.
PR	12-JUN-1998;	98US-0089155.
XX		
PA	(UYAL-) UNIV ALBERTA.	
PI	Hodges RS, Irvin RT;	
XX		
DR	WPI: 2000-106013/09.	
DR	N-PSDB: AAZ29534.	
PT		
PP	Composition for treating or preventing Pseudomonas aeruginosa infection comprising pilin protein that can not self-assemble -	
XX		
PS	Claim 9; Fig 1A; 32pp; English.	
CC		
CC	The present sequence is the modified K122 pilin protein from	
CC	P. aeruginosa. The N-terminal 1-28 residues are deleted from K122 strain	
CC	pilin protein. The modified protein thus lacks a critical alpha-helical	
CC	forming portion. This prevents oligomerisation of pilin protein necessary	
CC	for attachment to the host cell during infection. The first five	
CC	amino acid residues are not native to the K122 sequence, but are derived	
CC	from an intrinsic coding sequence of the expression vector. The	
CC	C-terminal residue is the Pro residue immediately upstream of the stop	
CC	OGH codons. The modified pilin protein is useful in treatment and	
CC	prophylaxis for individuals at risk of pseudomonas infection, e.g.	
CC	cystic fibrosis patients, burn patients, and severe neutropenic patients.	
XX		
\$Q	Sequence 129 AA;	
	Query Match 17.9%; Score 109.5; DB 21; Length 129;	
	Best Local Similarity 31.2%; Pred. No. 0.0003:	
	Matches 40; Conservative 18; Mismatches 51; Indels 19; Gaps 7;	
OY	1 ALEGTFFARSEGASALATINPLKTTVEESLSRGIAGSKIKIGTASTATETVAGVEPDPAN 60	
Dd	1 alegtfefarsegasermtlasgiktvdsifsgd--gs-----cpntaat--aglekld 51	
OY	61 KLGVAVAIIED-----SGAGDITTFPG-TGTSSP-KNATKYITLNRADG--VWACKST 110	
Dd	52 lngkvavavttvgtaaaaggctivatmksadvatplrgktlcltlnadkgsytwactsn 111	
OY	111 QDPMFTPK 118	
Dd	112 adnkylpk 119	
RESULT 10		
AAR38503		
ID	AAR38503 standard; protein; 53 AA.	
AC	AAR38503;	
DT	28-OCT-1993 (first entry)	
DE	P. aeruginosa pilin protein submolecular unit.	
KW	Antibodies: whole pili binding; basis: vaccine; bacterial infection;	
KX	rhumnant footrot infection; sheep; type IV pillated bacteria.	
OS	Pseudomonas aeruginosa.	

PN W09311791-A.
 PS 24-JUN-1993.
 XX
 XX
 PF 17-DEC-1992; 92WO-US11085.
 XX
 PR 18-DEC-1991; 91US-0809762.
 XX
 PA (UYOR-) UNIV OREGON HEALTH SCI.
 XX
 PI Smith AM;
 XX
 DR WPI: 1993-213824/26.
 XX
 XX Antigenic preparation - stimulates production of antibodies binding
 PT to pilin protein of type IV pillated bacteria, useful in
 PT vaccine compsn.
 XX
 PS Claim 18; Page 27; 44pp; English.
 XX
 CC The sequence is that of a submolecular unit of Pseudomonas aeruginosa
 CC pilin protein which corresponds to at least one epitope common to
 CC structural pilin proteins of Type IV pillated bacteria. It is
 CC capable of eliciting antibodies (Abs) which bind to whole pill of
 CC type IV bacteria. The ability of the submolecular unit to produce
 CC Abs which bind to whole pill provides the basis for vaccines against
 CC type IV bacterial infections, e.g. footrot infection in ruminants.
 CC
 SO Sequence 53 AA;
 Query Match 16.3%; Score 99.5; DB 14; Length 53;
 Best Local Similarity 84.6%; Pred. No. 0.0011; Mismatches 0; Indels 1; Gaps 1;
 Matches 22; Conservative 3; Mismatches 0; Indels 1; Gaps 1;
 OY 8 ARSEGASALATINPKTYVESLSRG 33
 Db 29 arsegasal-svnpkltvealsrg 53
 RESULT 11
 AAY44383
 ID AAY44383 standard; Protein; 175 AA.
 XX
 AC AAY44383;
 XX
 DT 14-MAR-2000 (first entry)
 XX
 DE P.aeruginosa E coll-truncated K122 pilin protein.
 XX
 KW Modified K122 pilin protein; alpha-helical forming portion; E coll;
 KW Exemplary coll; coiled coll heterodimer; host cell-receptor site;
 KW Pseudomonas infection; cystic fibrosis; neutropenia.
 OS
 XX Pseudomonas aeruginosa.
 XX
 PN W0965511-A2.
 PD 23-DEC-1999.
 XX
 PF 11-JUN-1999; 99WO-CA00554.
 XX
 PR 12-JUN-1998; 98US-0089155.
 XX
 PA (UYAL-) UNIV ALBERTA.
 XX
 PI Hodges RS, Irvin RT;
 XX
 DR WPI: 2000-106013/09.
 DR N-PSDB: AAZ29542.
 XX
 PT Composition for treating or preventing Pseudomonas aeruginosa infection
 PT comprising pilin protein that can not self-assemble -

XX
 PS Claim 1; Fig 4B; 32pp; English.
 XX
 CC The present sequence encodes E coll truncated K122 pilin protein from
 CC P.aeruginosa. The first 15-40 residues of the N-terminal peptide region
 CC is replaced by a peptide segment capable of forming a coiled-coil
 CC heterodimer with an oppositely charged peptide segment which can form
 CC dimeric structures. These proteins are less inflammatory due to reduced
 CC degree of mobilisation of host-cell receptor sites. This prevents
 CC oligomerisation of pilin protein necessary for attachment to the host
 CC cell during infection. The modified pilin protein is useful in treatment
 CC and prophylaxis for individuals at risk of Pseudomonas infection,
 CC e.g. cystic fibrosis patients, burn patients, and severe neutropenic
 CC patients.
 CC
 SO Sequence 175 AA;
 Query Match 14.9%; Score 91; DB 21; Length 175;
 Best Local Similarity 29.8%; Pred. No. 0.047; Mismatches 52; Indels 22; Gaps 8;
 Matches 39; Conservative 18; Mismatches 52; Indels 22; Gaps 8;
 OY 1 ALE---CTEPAREGASALATINPKTYVESLSRGISGSKIRIGTASTATYAGVGP 57
 Db 44 aleksgggetarqasermtlasgltkvsdlfsqd--gs-----cpantaaat--agiek 94
 OY 58 DANKLGIVAVIED-----SGAGDITFTFO-TGTSSP-KNATKYITLNRITADG--VWAC 107
 Db 95 ddingkyvakvtlgtgtaasggtlvatmkasdvatpirtgkltlignadkgsylwac 154
 OY 108 KSTQDPMETPK 118
 Db 155 tsnadnkylpk 165
 RESULT 12
 AAR25900
 ID AAR25900 standard; Protein; 17 AA.
 XX
 AC AAR25900;
 XX
 DT 20-JAN-1993 (first entry)
 XX
 DE P.aeruginosa PAO pilin C-terminal sequence.
 XX
 KW Strain PAO; pulmonary epithelial cell.
 KW
 XX Pseudomonas aeruginosa.
 OS
 XX
 FH Key Location/Qualifiers
 FT Region 7..13 "peptides comprising at least this
 FT /note= "antigenic subsequence are also claimed"
 XX
 PN W09212169-A.
 PD 23-JUL-1992.
 XX
 PF 24-DEC-1991; 91WO-CA00459.
 XX
 PR 04-JAN-1991; 91US-0638492.
 XX
 PA (SVNT-) SYNTHETIC PEPTIDES INC.
 XX
 PI Doig PC, Hodges RS, Irvin RT, Lee KK, Paranchych W;
 PI Pariml SA, Wong WY, Zoutmon DE;
 XX
 DR WPI: 1992-268611/32.
 DR N-PSDB: AAO27083.
 XX
 PT C-terminal portion of Pseudomonas aeruginosa pilin protein -
 PT useful as a vaccine against non-Pseudomonas cross-reactive
 PT microorganisms for preventing bacterial and fungal infections

XX Claim 3(Amended): Page 72; 96pp; English.

PS This sequence is the C-terminal amino acid sequence of pilin
CC from the P.aeruginosa strain PAO, one of 10 strains which were
CC investigated. The PAO peptide is classified in a group with
CC C-terminal peptides containing 14 residues from Cys to Cys and
CC is cross-reactive with surface peptides in certain bacteria and
CC fungi. The peptides bind specifically to pulmonary epithelial cells.
CC See also AAR25828 and AAR25901-R25908.

XX Sequence 17 AA;

Query Match 14.7%; Score 90; DB 13; Length 17;
Best Local Similarity 94.1%; Pred. No. 0.0023;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 106 ACKSTODPMFTPKGSDN 122
DB 1 ackstqdpmtfpxgcdn 17

RESULT 13

AAR6704
ID AAR6704 standard; peptide; 17 AA.

XX AAR6704;

XX 26-JUN-1996 (first entry)

XX Pilin derived peptide, PAO.

XX Epitope: exoenzyme; ExoS; enzymatic/cytotoxic protein; PK99H; MCAL;
KW P. aeruginosa; adhesin; monoclonal antibody; buccal epithelial cell;
KW cell surface receptor; adhesion domain; pilin protein; vaccine;
KW immunisation; infection; targeted drug delivery; carcinoma;
KW pulmonary epithelial cell.

XX Pseudomonas aeruginosa.

XX US5468484-A.

XX 21-NOV-1995.

XX 25-JUN-1991; 91US-0721759.

XX 28-JUN-1993; 93US-0084739.

XX 25-JUN-1991; 91US-0721759.

XX (SPIS-) SPI SYNTHETIC PEPTIDES INC.

XX Hodges RS, Irvin RT, Paranchych W, Sokol PA, Woods DE;

XX WPI: 1996-010050/01.

XX Preventing P.aeruginosa infections by passive immunisation - using
PT monoclonal antibody reactive with exoS and pilin peptide epitope(s)
XX
PS Claim 1; Column 31; 26pp; English.

CC The sequences given in AAR6702-08 are peptides which have the same
CC immunoreactivity as the peptide sequence given in AAR6701. These
CC peptides are derived from the P. aeruginosa pilin protein. The peptide
CC of the invention is derived from the exoenzyme, ExoS. ExoS is an
CC enzymatic/cytotoxic protein present on the surface of P. aeruginosa
CC cells. It is also an adhesin. It demonstrates immunospecific binding
CC to monoclonal antibodies PK99H and MCAL. The ExoS derived peptide has
CC the ability to block binding of P. aeruginosa to buccal epithelial cells
CC by blocking a cell surface receptor. It is homologous to known adhesion
CC domains in the P. aeruginosa pilin protein, esp. the region 131-143.
CC These peptides may be used in vaccines to provide active immunisation
CC against infection by P. aeruginosa or related organisms. They can also

CC be used for targeted drug delivery to pulmonary epithelial cells, e.g.
CC for treating carcinoma they are coupled to photoactivatable
CC chemotherapeutic agents.

XX Sequence 17 AA;

Query Match 14.7%; Score 90; DB 17; Length 17;
Best Local Similarity 94.1%; Pred. No. 0.0023;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 106 ACKSTODPMFTPKGSDN 122
DB 1 ackstqdpmtfpxgcdn 17

RESULT 14

AA49351
ID AA49351 standard; peptide; 17 AA.

XX AA49351;

XX 14-MAR-2000 (first entry)

XX P. aeruginosa PAO pilin peptide native sequence.
XX Vaccine; P. aeruginosa; pilin; Pseudomonas infection; PAO;
KW antibacterial.

XX Pseudomonas aeruginosa.

XX WO9557142-A2.

XX 11-NOV-1999.

XX 06-MAY-1999; 99WO-CA00366.

XX 06-MAY-1998; 98US-0084444.

XX (UYAL-) UN V ALBERTA.

XX Hodges RS, Irvin RT, Cachia PJ;

XX WPI: 2000-072227/06.

XX Novel vaccine used to prevent Pseudomonas aeruginosa infection -
PT disclosure; Fig 1; 21pp; English.

CC The invention provides a peptide vaccine against P. aeruginosa that
CC comprises a pilin peptide conjugated to a carrier protein. The pilin
CC peptide has one of the four sequences selected from AA49352-355. The
CC vaccine is used to prevent Pseudomonas infections. The present sequence
CC represents a native fragment of pilin peptide from P. aeruginosa strain
CC PAO.

XX Sequence 17 AA;

Query Match 14.7%; Score 90; DB 21; Length 17;
Best Local Similarity 94.1%; Pred. No. 0.0023;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 106 ACKSTODPMFTPKGSDN 122
DB 1 ackstqdpmtfpxgcdn 17

RESULT 15

AA49367
ID AA49367 standard; peptide; 17 AA.

XX AA49367;

```

XX
DT 14-MAR-2000 (first entry)
XX
DE Cell surface binding domain from P. aeruginosa pilin strain PAO.
XX
KW Vaccine; P. aeruginosa; pilin; Pseudomonas infection; antibacterial;
XX cell surface binding domain.
XX
OS Pseudomonas aeruginosa.
XX
PN WO957142-A2.
XX
PD 11-NOV-1999.
XX
PF 06-MAY-1999; 99WO-CA00366.
XX
PR 06-MAY-1998; 98US-0084444.
XX
PA (UYAL-) UNIV ALBERTA.
XX
PI Hodges RS, Irvin RT, Cachla PJ;
XX
DR WPI; 2000-072227/06.
XX
PT Novel vaccine used to prevent Pseudomonas aeruginosa infection -
XX
PS Disclosure; Fig 11; 21pp; English.
XX
CC The invention provides a peptide vaccine against P. aeruginosa that
CC comprises a pilin peptide conjugated to a carrier protein. The pilin
CC peptide has one of the four sequences selected from AY49352-355. The
CC vaccine is used to prevent Pseudomonas infections. The present sequence
CC represents a cell surface binding domain from P. aeruginosa pilin strain
CC PAO.
XX
SQ Sequence 17 AA;

Query Match 14.7%; Score 90; DB 21; Length 17;
Best Local Similarity 94.1%; Pred. No. 0.0023;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 106 ACKSTODPMFTPKGSDN 122
   |||||||||||||
Db 1 ackstgdpmtfpgkcdn 17

```

Search completed: February 8, 2002, 15:24:32
 Job time: 77 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 8, 2002, 15:25:55 ; Search time 37.87 Seconds

(without alignments)
245,400 Million cell updates/sec

Title: US-09-865-159-6

Perfect score: 612
1 ALEGTGFARSEGASALATIN.....GWACKSTODPMETPKGSDN 122

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR:68:*
2: PIR1:*
3: PIR2:*
4: PIR3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	568	92.8	149	2 A25023	type 4 fimbrial pr
2	426	69.6	150	2 A43504	pilin precursor -
3	419	68.5	150	2 B24603	fimbrial protein -
4	290.5	47.5	150	1 YQSPA	fimbrial protein p
5	116.5	19.0	148	2 F82544	fimbrial protein x
6	114	18.6	167	2 C82077	fimbrial protein v
7	108.5	17.7	155	2 J10071	alpha-pilin - Mora
8	107	17.5	136	2 S52692	fimbrial protein -
9	105.5	17.2	157	2 A46566	pilin precursor -
10	104	17.0	156	2 S15267	fima protein - Dic
11	102.5	16.7	154	2 S04440	fimbrial protein -
12	102.5	16.7	154	2 B31105	fimbrial protein p
13	102	16.7	148	2 C82544	fimbrial protein x
14	100	16.3	135	2 S52693	fimbrial protein -
15	98.5	16.1	156	2 S15266	fima protein - Xanth
16	88	14.4	159	2 A47699	type 4 pilin - Elk
17	84.5	13.8	502	2 F31751	protein kinase cat
18	84	13.7	164	2 A42460	fimbrial protein Q
19	84	13.7	595	2 B48658	flagellin - Escher
20	82	13.4	158	2 A55851	prepilin - Moraxel
21	80.5	13.2	498	1 FLEC	flagellin - Escher
22	80	13.1	136	2 D36961	pilin pila precurs
23	77.5	12.7	161	2 S15262	fima protein - Dic
24	77.5	12.7	937	2 S58135	hypally regulated
25	77	12.6	1036	2 A29832	HPI layer surface
26	76	12.4	413	2 A46183	heat shock protein
27	75.5	12.3	156	2 A41490	pilin precursor -
28	75.5	12.3	252	2 H72469	hypothetical prote
29	75.5	12.3	1275	2 T33369	hypothetical prote

30	75	12.3	160	2 T23995	hypothetical prote
31	75	12.3	457	2 H70820	hypothetical glyci
32	75	12.3	1200	2 T17404	hyalin - sea urchi
33	74.5	12.2	157	2 A31105	fimbrial protein p
34	74.5	12.2	298	2 T64138	adhesin homolog HI
35	74	12.1	157	2 A24434	beta fimbrial prot
36	74	12.1	350	2 F86804	basic membrane pro
37	74	12.1	807	2 C85025	hypothetical prote
38	73.5	12.0	512	2 A70569	probable cpsa prot
39	73.5	12.0	668	2 J02354	capsid protein - f
40	73.5	12.0	1026	1 TRP74	tail fiber protein
41	73	11.9	464	2 E83834	flagellin BH477 l
42	72.5	11.8	160	2 A57167	pilin precursor -
43	72.5	11.8	161	2 S15268	fima protein - Dic
44	72.5	11.8	326	2 T50128	hypothetical serin
45	72.5	11.8	1033	2 F71256	conserved hypothet

ALIGNMENTS

```

RESULT 1
type 4 fimbrial precursor Pila PA4525 [imported] - Pseudomonas aeruginosa (strain PA
N:Alternate names: pilin
C:Species: Pseudomonas aeruginosa
C:Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 31-Dec-2000
C:Accession: A25023; H83080
R:Sastiy, P.A.; Finlay, B.B.; Pastoske, B.L.; Paranchych, W.; Pearlstone, J.R.; Sml
J. Bacteriol. 164, 571-577, 1985
A:Title: Comparative studies of the amino acid and nucleotide sequences of pilin der
A:Reference number: A25023; MUID:8603611
A:Accession: A25023
A:Molecule type: DNA
A:Residues: 1-149 <SAS>
R:Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.;
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic p
A:Reference number: A82950; MUID:20437337
A:Accession: H83080
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-149 <STO>
A:Cross-references: GB:AE004866; GB:AE004091; NID:g9950760; PIDN:AA07913.1; GSPDB:G
A:Experimental source: strain PA01
C:Genetics:
A:Gene: pilA; PA4525
C:Superfamily: gonococcal fimbrial protein
C:Keywords: methylated amino end
F:7/Modified site: methylated amino end (Phe) (in mature form) #status predicted
Query Match 92.8%; Score 568; DB 2; Length 149;
Best Local Similarity 98.3%; Pred. No. 1.9e-45;
Matches 113; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 8 ARSEASALATNPPLKTYEESLSRGISGSKRIKIGTTASTATETAGVAGVPPDNKLGIVAV 67
DB 35 ARSEASALATNPPLKTYEESLSRGISGSKRIKIGTTASTATETAGVAGVPPDNKLGIVAV 94
OY 68 AIEDSGAGDITFTFTGTSSPPKNAKVTITLNPADGVMACKSTODPMETPKGSDN 122
DB 95 AIEDSGAGDITFTFTGTSSPPKNAKVTITLNPADGVMACKSTODPMETPKGSDN 149
RESULT 2
type 4 fimbrial precursor - Pseudomonas aeruginosa
C:Species: Pseudomonas aeruginosa
C:Date: 21-Oct-1992 #sequence_revision 21-Oct-1992 #text_change 29-Jan-1999

```

C:Accession: A43504
 R:Pasloske, B.L.; Joffe, A.M.; Sun, Q.; Volpel, K.; Paranchych, W.; Eftekhar, F.; Speert
 Infect. Immun. 56, 665-672, 1988
 A:Title: Serial isolates of *Pseudomonas aeruginosa* from a cystic fibrosis patient have
 A:Reference number: A43504; MUID:86138467
 A:Accession: A43504
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-150 <PAS>
 A:Cross-references: GB:M24281
 C:Superfamily: gonococcal fimbril protein
 C:Keywords: methylated amino end
 F:7/Modified site: methylated amino end (Phe) (in mature form) #status predicted

Query Match 69.6%; Score 426; DB 2; Length 150;
 Best Local Similarity 75.9%; Pred. No. 2,4e-32;
 Matches 85; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

OY 8 ARSBSALATINPLKTTVESLSRGISGKIKITGTTASTATTETAGVDPDANKLGIVAV 67
 Db 35 ARSBSALATINPLKTTVESLSRGISGKIKITGTTASTATTETAGVDPDANKLGIVAV 67
 OY 68 AIEDSGADITFTFTGTSPPKNAKVTITNRTADGWACKSTQDDPMTFG 119
 Db 95 TIKDTGDTIKFNATGSSPKNKGRTITLNRTRAEGWTCSTQDEMFIPKG 146

RESULT 3
 B24603
 Fimbril protein - *Pseudomonas aeruginosa* (strain PA103)
 C:Species: *Pseudomonas aeruginosa*
 C:Date: 11-Dec-1987 #sequence-revision 11-Dec-1987 #text-change 26-Aug-1999
 C:Accession: B24603
 R:Johnson, K.; Parker, M.L.; Lory, S.
 J. Biol. Chem. 261, 15703-15708, 1986
 A:Title: Nucleotide sequence and transcriptional initiation site of two *Pseudomonas aer*
 A:Reference number: A24603; MUID:87057209
 A:Accession: B24603
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-150 <JOH>
 A:Cross-references: GB:M14850; GB:J02609; GB:J02682; NID:g151475; PIDN:AAA25953.1; PID:g
 C:Superfamily: gonococcal fimbril protein
 C:Keywords: methylated amino end
 F:7/Modified site: methylated amino end (Phe) (in mature form) #status predicted

Query Match 68.5%; Score 419; DB 2; Length 150;
 Best Local Similarity 75.0%; Pred. No. 1,1e-31;
 Matches 84; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

OY 8 ARSBSALATINPLKTTVESLSRGISGKIKITGTTASTATTETAGVDPDANKLGIVAV 67
 Db 35 ARSBSALATINPLKTTVESLSRGISGKIKITGTTASTATTETAGVDPDANKLGIVAV 67
 OY 68 AIEDSGADITFTFTGTSPPKNAKVTITNRTADGWACKSTQDDPMTFG 119
 Db 95 TIKDTGDTIKFNATGSSPKNKGRTITLNRTRAEGWTCSTQDEMFIPKG 146

RESULT 4
 Y0PSPA
 Fimbril protein precursor - *Pseudomonas aeruginosa* (strain PAK)
 N:Alternate names: pilin
 C:Species: *Pseudomonas aeruginosa*
 C:Date: 14-Nov-1983 #sequence-revision 16-Oct-1998 #text-change 16-Jul-1999
 C:Accession: A24603; A28780; A03497
 R:Johnson, K.; Parker, M.L.; Lory, S.
 J. Biol. Chem. 261, 15703-15708, 1986
 A:Title: Nucleotide sequence and transcriptional initiation site of two *Pseudomonas aer*
 A:Reference number: A24603; MUID:87057209
 A:Accession: A24603

A:Molecule type: DNA
 A:Residues: 1-150 <JOH>
 A:Cross-references: GB:M14849; GB:J02609; NID:g151479; PIDN:AAA25953.1; PID:g151480
 R:Pasloske, B.L.; Finlay, B.B.; Paranchych, W.
 FEMS Lett. 183, 408-412, 1985
 A:Title: Cloning and sequencing of the *Pseudomonas aeruginosa* PAK pilin gene.
 A:Reference number: A28780; MUID:85180008
 A:Accession: A28780
 A:Molecule type: DNA
 A:Residues: 1-149 'R' <PSK>
 A:Cross-references: GB:X02402; GB:M11462; NID:g45331; PIDN:CAA26248.1; PID:g45332
 R:Sastiy, P.A.; Pearlstone, J.R.; Smillie, L.B.; Paranchych, W.
 FEMS Lett. 151, 253-256, 1983
 A:Title: Amino acid sequence of pilin isolated from *Pseudomonas aeruginosa* PAK.
 A:Reference number: A03497; MUID:83158129
 A:Accession: A03497
 A:Molecule type: protein
 A:Residues: 7-90 'S', '91-100', 'DTA', '104-150' <SAS>
 A>Note: the pil from which this protein was isolated are polar flexible filaments o

C:Superfamily: gonococcal fimbril protein
 C:Keywords: fimbril; methylated amino end; pilin formation
 F:1-6/Domain: propeptide #status predicted <PRO>
 F:7-150/Product: fimbril protein #status predicted <MAT>
 F:7/Modified site: methylated amino end (Phe) (in mature form) #status predicted

Query Match 47.5%; Score 290.5; DB 1; Length 150;
 Best Local Similarity 57.8%; Pred. No. 7,4e-20;
 Matches 67; Conservative 11; Mismatches 31; Indels 7; Gaps 4;

OY 8 ARSBSALATINPLKTTVESLSRGISGKIKITGTTASTATTETAGVDPDANKLGIVAV 65
 Db 35 ARSBSALASVNPPLKTTVEALSRSWS--VKSGTGEADTKKEVPLGVAADANKIGTI 91

OY 66 AVALIEDS-GADITFTFTGTSPPKNAKVTITNRTADGWACKSTQDDPMTFG 119
 Db 92 ALKRDPAIDGTDITLFTFMGAGPKNKGRTITLNRTRAEGLMKTCTSDPDQFIPKG 147

RESULT 5
 F82544
 Fimbril protein XF2542 [imported] - *Xylella fastidiosa* (strain 945c)
 C:Species: *Xylella fastidiosa*
 C:Date: 18-Aug-2000 #sequence-revision 20-Aug-2000 #text-change 02-Sep-2000
 C:Accession: F82544
 R:Anonymous, The *Xylella fastidiosa* Consortium of the organization for Nucleotide Se
 Nature 406, 151-157, 2000
 A:Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.
 A:Reference number: A82515; MUID:20365717
 A>Note: for a complete list of authors see reference number A59328 Below
 A:Accession: F82544
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-148 <SIM>
 A:Cross-references: GB:AE004061; GB:AE003849; NID:g9107747; PIDN:AAE85339.1; GSPDB:G
 A:Experimental source: strain 945c
 R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R
 Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carre
 as-Neto, E.; Docena, C.; El-Dorri, H.; Facinanci, A.P.; Ferreira, A.J.S.
 Submitted to GenBank, June 2000
 A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; F
 J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kurame, E.E.; L
 chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martin
 A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C
 F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, C
 Rodrigues, V.; Rosa, A.C.; de M.; de Rosa Jr.; V.E.; de Sa, R.G.; Santelli, R.V.; Sawe
 M.; Tsunako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.
 A:Reference number: A59328
 A:Contents: annotation
 C:Genetics: A:Gene: XF2542

Matches 35; Conservative 18; Mismatches 42; Indels 21; Gaps 5;

Y 8 ARSEGASALATINPLKTVEESLSRG--IACS-----KIKIGTASTATETTYAGVEPDA 59

Db 35 ARTQVRAVSEVSAKLTAAESAILLECKREIVSSATPKQTQYDIGFTFESTLLD----- 85
 ANSEGGASALAIINPLKTIIVEESLSRG--IAGS-----KIKIGTASATETFAAGVEDDA 59

QY 60 NKLGVIAVAIEDSGAGDITFTFQTCGSSPKNATK--VITLNRADGWACKSTQDP 113

D6 : : : : :
86 -GSGKSQIQVTDNDGDGTVELVATLGKSS-GSAIKGAIVTVSRKNDGVWNNCKITKTP 139

RESULT 12

B3105

C;Species: *Pseudomonas aeruginosa*
C;Strain: *Pseudomonas aeruginosa* (strain P1)
C;Accession: *Pseudomonas aeruginosa* (strain P1)
C;Date: 31-Mar-1990 #sequence revision 31-Mar-1990 #

C/Accession: B31105
SequenceRevision 31-Mar-1990
#text_change 08-Oct-1999
C/Pasloske, B.L.; Sastuv, P.A.; Einlan, D.D.; Bernasconi, R.

J. Bacteriol. 170, 3738-3741, 1988

A; Accession: B31105
A; Reference number: A91879; MUID: 88298689

A: Molecule type: DNA
A: Residues: 1-154 <PAS>

A; Cross-references: GB:M21652; NID:g151471; PIRN:AAC63060.1; PID:g151472
C; Superfamily: qonococcal fimbrial protein

E;1-6/Domain: signal sequence #status predicted <SIG>
F;7-154/Product: fibriaral protein #status predicted <MAN>

[illegible]

Query Match	16.7%	Score 102.5;	DB 2;	Length 154;
Best Local Similarity	30.2%	Pred. No. 0.016;		

Matches	35;	Conservative	18;	Mismatches	42;	Indels	21;	Gaps	5;
---------	-----	--------------	-----	------------	-----	--------	-----	------	----

```

8 ARSEGASALATINPKTVEESLSRG--IAGS-----KIKICTTSTATEFYAGVEPDA 59
||:: ||:::||| ||::||| |

```

35 ARTQVTRAVSEVSALKTAESAILEGKEIVSSATPKDTQYDIDIGFTESLID----- 85

60 NKLGI A V A L E D S G A D I T F T Q T G T S S P K N A T K - V I T L N R T A D C W A C K S T Q D P 113

86 -GSGKSOIQVTDNKGDTVELVATLGSS-GSAIRGAVITVSRKNDGVNCKITKP 139

RESULT 13

EFimbrin protein, XP2539 [imported] - Xylella fastidiosa (strain 9a5c)
382544

Species: *Xylella fastidiosa*
Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000

3,anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequences, 1999, accession: C82544

Figure 406, 151-157, 2000

*,Note: for a complete list of authors see reference number A53328 below

```

      ,accession: C02344
      ,Status: preliminary
      ,Molecule_type: DNA

```

```

;Residues: 1-148 <SIM>
;Cross-references: CD, AF000661, CD, AF000661,
;Molecule type: DNA

```

Experimental source: strain 9a5c
References: GB:AE00V061; GB:AE003849; NID:g9107747; GSP:PIDN:AAFB5336.1; Simonson, A J G., Bettsch, P C.,

[illegible]

Submitted to Genbank, June 2000

D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Machado, M.A.; Madeira, A.M.B.N.; Madeira, P.M.; Oliveira, V.C.; Passaglia, J.S.; Franca, S.C.; Franco, M.C.

Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyak

Autores: da Silva, A.C.P.; da Silva, V.E.; de Sa, R.G.; Santelli, R.V.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; palmieri, J.; Ramos, L.N.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; palmieri, J.; Ramos, L.N.;

Reference number: A50320
Tsunako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, W.A.; da Silva, A.M.; da Silva, F.R.; da Silva, H.C.N.; da Silva, J.R.

REFERENCE NUMBER: A55340

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 8, 2002, 15:34:21 ; Search time 22.14 Seconds

(without alignments)
202.037 Million cell updates/sec

Title: US-09-865-159-6

Perfect score: 612
Sequence: 1 ALEGTAFARSECASALATIN.....GYWACKSTQDPMTETKSGSDN 122

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SWISSProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	568	92.8	149	1	FMPO_PSEAE
2	426	69.6	150	1	FMCD_PSEAE
3	419	68.5	150	1	FMP3_PSEAE
4	290.5	47.5	150	1	FMPA_PSEAE
5	108.5	17.7	159	1	FMI_MORBO
6	103	16.8	156	1	FMAH_BACNO
7	102.5	16.7	154	1	FM12_PSEAE
8	102.5	16.7	154	1	FMK1_PSEAE
9	98.5	16.1	156	1	FMAI_BACNO
10	88	14.4	159	1	ECRA_EIKCO
11	84.5	13.8	302	1	KDC2_DROME
12	80.5	13.2	497	1	FLIC_ECOLI
13	80	13.1	136	1	FMWC_PSEPU
14	77.5	12.7	161	1	FMAE_BACNO
15	77	12.6	1036	1	HP12_DEIRA
16	75.5	12.3	3358	1	PGCV_MOUSE
17	75	12.3	160	1	YRNS_CAEEL
18	74.5	12.2	157	1	FMP1_PSEAE
19	74	12.1	157	1	FMO_MORBO
20	73.5	12.0	937	1	HYR1_CANAL
21	73.5	12.0	1026	1	VG37_BPT4
22	72.5	11.8	160	1	FMAI_BACNO
23	72.5	11.8	161	1	FMAI_BACNO
24	72	11.8	128	1	FMAI_BACNO
25	72	11.8	697	1	YHFO_YEAST
26	72	11.8	893	1	PER_PERAM
27	71	11.6	658	1	STC1_STANU
28	71	11.6	715	1	STC2_STANU
29	71	11.6	781	1	PBPB_HATIN
30	70.5	11.5	162	1	FMAE_BACNO
31	70.5	11.5	216	1	YC97_SCHPO
32	70	11.4	488	1	FLIC_PSEAE
33	69.5	11.4	272	1	OSAT_BORBU

34	69.5	11.4	314	1	YG98_MYCTU
35	69.5	11.4	378	1	ELYA_BACSP
36	69.5	11.4	952	1	IF41_YEAST
37	69.5	11.4	1043	1	EE3A_YEAST
38	69.5	11.4	1140	1	YM6E_YEAST
39	69.5	11.3	881	1	YJH8_YEAST
40	68.5	11.2	282	1	PRTA_ASPNG
41	68.5	11.2	384	1	FTS2_BUCAL
42	68.5	11.2	415	1	SCB2_CAEEL
43	68.5	11.2	891	1	ACON_LEGPN
44	68.5	11.2	1043	1	EE3B_YEAST
45	68.5	11.2	1047	1	HIRA_DROME

ALIGNMENTS

RESULT 1
FMPO_PSEAE STANDARD; PRT; 149 AA.
ID FMPO_PSEAE
AC P04739;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE FIMBRIAL PROTEIN PRECURSOR (PILIIN) (STRAIN PAO).
GN PIIA OR FIIM OR PA4525.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
NCBI_TaxID=287;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=PAO;
RC MEDLINE=86033611; PubMed=2997119;
RX Sastry P.A., Finlay B.B., Pastoske B.L., Paranchych W.,
RA Pearlstone J.R., Smillie L.B.;
RT "Comparative studies of the amino acid and nucleotide sequences of
RT pili derived from Pseudomonas aeruginosa PAO and PAO.";
RL J. Bacteriol. 164:571-577(1985).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=ATCC 15692 / PAOI;
RC MEDLINE=20437337; PubMed=10984043;
RX Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Huffnagle W.O., Kowalik D.J., Lagrou M.,
RA Gader R.L., Goltzy L., Tolentino E., Westbrook-Madman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Salier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PAOI, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
[3]
RN MUTAGENESIS OF GIU-11.
RP MEDLINE=93321167; PubMed=8330261;
RX Macdonald D.L., Pastoske B.L., Paranchych W.;
RT "Mutations in the fifth-position glutamate in Pseudomonas aeruginosa
RT pili affect the transmethylation of the N-terminal phenylalanine.";
RL Can. J. Microbiol. 39:500-505(1993).
[4]
RN STRUCTURE BY NMR OF 132-149.
RP MEDLINE=96110702; PubMed=8845350;
RX Campbell A.P., McInnes C., Hodges R.S., Sykes B.D.;
RT "Comparison of NMR solution structures of the receptor binding
RT domains of Pseudomonas aeruginosa pili strains PAO, KB7, and PAO;
RT implications for receptor binding and synthetic vaccine design.";
RL Biochemistry 34:16255-16268(1995).
CC -I- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
CC NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
CC CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
CC CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.
CC -I- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).

DR EMBL: M11323; AAA25954.1;
 DR EMBL: AE004866; AAG07913.1;
 DR PIR: A25023; A25023.
 DR PDB: IPAN: 29-JAN-96.
 DR PDB: IPAO: 29-JAN-96.
 DR InterPro: IPR001082; PiliN.
 DR InterPro: IPR001120; Prok_N_methyltn.
 DR Pfam: PF00114; PiliN; 1.
 DR ProDom: PD000666; PiliN; 1.
 DR PROSITE: PS00409; PROKAR_NTER METHYL; 1.
 DR Fimbrin; Methylation; 3D-structure; Complete proteome.
 FT PROPEP 1 6
 FT CHAIN 7 149 FIMBRIAL PROTEIN.
 FT MOD_RES 7 7 METHYLATION (BY SIMILARITY).
 FT DISULFID 134 147 BY SIMILARITY.
 FT MOTAGN 11 11 E->A: METHYLATION OF PHE-7 DECREASED AND
 FT LOSS OF PILI ASSEMBLY.
 SQ SEQUENCE 149 AA; 15512 MW; 98EC8A6F7B02214 CRC64;

Query Match 92.8%; Score 568; DB 1; Length 149;
 Best Local Similarity 98.3%; Pred. No. 1.5e-44;
 Matches 113; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 ARSEGASALATINPLKTTVEESLSRGISGSKIKIGTASTATETAGVGPDPANKLGIVAV 67
 DB 35 ARSEGASALATINPLKTTVEESLSRGISGSKIKIGTASTATETAGVGPDPANKLGIVAV 94

QY 68 AIEDSGAGITFTPTGTSSPKNATKVTILNRTADGVWACKSTODMPFKGSDN 122
 DB 95 AIEDSGAGITFTPTGTSSPKNATKVTILNRTADGVWACKSTODMPFKGSDN 149

RESULT 2
 FMCD_PSEAE STANDARD; PRT; 150 AA.
 AC P17837;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE FIMBRIAL PROTEIN PRECURSOR (PILIN) (STRAIN CD).
 GN PILA OR FIMA.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CD;
 RX MEDLINE=88138467; PubMed=2893774;
 RA Pasloske B.L., Joffe A.M., Sun Q., Volpel K., Paranchych W.,
 RA Efekhar F., Speert D.P.,
 RT "Serial isolates of Pseudomonas aeruginosa from a cystic fibrosis
 RT patient have identical pilin sequences.";
 RL Infect. Immun. 56:665-672(1988).
 CC -1- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
 CC NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
 CC CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
 CC CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.
 CC -1- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY. ALMOST IDENTICAL
 CC TO PA103 PILIN.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
 CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).

DR EMBL: M24281; AAA25945.1; ALT_INIT.
 DR PIR: A43504; A43504.
 DR HSSP: P02973; INTL.
 DR InterPro: IPR001082; PiliN.
 DR InterPro: IPR001120; Prok_N_methyltn.
 DR Pfam: PF00114; PiliN; 1.
 DR ProDom: PD000666; PiliN; 1.
 DR PROSITE: PS00409; PROKAR_NTER METHYL; 1.
 DR Fimbrin; Methylation.
 FT PROPEP 1 6
 FT CHAIN 7 150 FIMBRIAL PROTEIN.
 FT MOD_RES 7 7 METHYLATION (BY SIMILARITY).
 FT DISULFID 134 147 BY SIMILARITY.
 SQ SEQUENCE 150 AA; 15743 MW; E14316996F270F3C CRC64;

Query Match 69.6%; Score 426; DB 1; Length 150;
 Best Local Similarity 75.9%; Pred. No. 9.1e-32;
 Matches 85; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

QY 8 ARSEGASALATINPLKTTVEESLSRGISGSKIKIGTASTATETAGVGPDPANKLGIVAV 67
 DB 35 ARSEGASALATINPLKTTVEESLSRGISGSKIKIGTASTATETAGVGPDPANKLGIVAV 94

QY 68 AIEDSGAGITFTPTGTSSPKNATKVTILNRTADGVWACKSTODMPFKGSDN 119
 DB 95 TIKQIDGIVKTFPTGTSSPKNATKVTILNRTADGVWACKSTODMPFKGSDN 146

RESULT 3
 FMCD_PSEAE STANDARD; PRT; 150 AA.
 AC P08015;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE FIMBRIAL PROTEIN PRECURSOR (PILIN) (STRAIN PA103).
 GN PILA OR FIMA.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PA103;
 RX MEDLINE=87057209; PubMed=2410961;
 RA Johnson K., Parker M.L., Lory S.;
 RT "Nucleotide sequence and transcriptional initiation site of two
 RT Pseudomonas aeruginosa pilin genes.";
 RL J. Biol. Chem. 261:15703-15708(1986).
 CC -1- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
 CC NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
 CC CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
 CC CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.
 CC -1- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY. ALMOST IDENTICAL
 CC TO CDI PILIN.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).

DR EMBL: M14850; AAA25953.1;
 DR PIR: B24603; B24603.
 DR HSSP: P02973; INTL.

```

DR InterPro: IPR001082; Piliin.
DR InterPro: IPR001120; Prok_N_methyltn.
DR Pfam: PF00114; Piliin; 1.
DR ProDom: PD000666; Piliin; 1.
DR ProSITE: PS00409; PROKAR_NTER_METHYL; 1.
KW Fimbria; Methylation.
FT PROPER 1 6
FT CHAIN 7 150 FIMBRIAL PROTEIN.
FT MOD_RES 7 7 METHYLATION (BY SIMILARITY).
FT DISULFID 134 147 BY SIMILARITY.
SO SEQUENCE 150 AA; 15799 MW; DBDAB68453D4DC85 CRC64;

Query Match 68.5%; Score 419; DB 1; Length 150;
Best Local Similarity 75.0%; Pred. No. 3.9e-31;
Matches 84; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

QY 8 ARSEGASALATINPLKTTVEESLSRGISGKIKIGTTASTATETAGVGPDPANKLGIVAV 67
Db 35 ARSEGASALATINPLKTTVEESLSRGISGKILGTTASTADTTVGVGIDEXANKLGIVAV 94

QY 68 AIEDSGAGDITFTTQGTSSPKNATKVTTLNRTADGWACKSTODPMFTPKG 119
Db 95 TIKTGTGDTIKFNATGSSPKNMGRETLNRTAGVWTCISTQDEMTIPKG 146

RESULT 4
FMPE_PSEAE 3
ID FMPE_PSEAE STANDARD; PRT; 150 AA.
AC P02973; 053390;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE FIMBRIAL PROTEIN PRECURSOR (PILIN) (STRAIN PAK).
GN PILA OR FIMA.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP STRAIN=PAK;
RC MEDLINE=87057209; PubMed=2430961;
RX MEDLINE=85180008; PubMed=2985436;
RA Pasloske B.L., Finlay B.B., Paranchych W.;
RT "Cloning and sequencing of the Pseudomonas aeruginosa PAK pilin
gene.";
RL FEBS Lett. 183:408-412(1985).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=PAK;
RX MEDLINE=87057209; PubMed=2430961;
RA Johnson K., Parker M.L., Lory S.;
RT "Nucleotide sequence and transcriptional initiation site of two
Pseudomonas aeruginosa pilin genes.";
RL J. Biol. Chem. 261:15703-15708(1986).
RN [3]
RP SEQUENCE OF 7-150.
RC STRAIN=PAK;
RX MEDLINE=83158129; PubMed=6131838;
RA Sastri P.A., Pearlstone J.R., Smillie L.B., Paranchych W.;
RT "Amino acid sequence of pilin isolated from Pseudomonas aeruginosa
PAK.";
RL FEBS Lett. 151:253-256(1983).
RN [4]
RP SEQUENCE OF 128-150 FROM N.A.
RX MEDLINE=94103636; PubMed=7903973;
RA IPTSG;
RT "A multicenter comparison of methods for typing strains of
Pseudomonas aeruginosa predominantly from patients with cystic
fibrosis. The International Pseudomonas aeruginosa Typing Study
Group.";
RL J. Infect. Dis. 169:134-142(1994).
RN [5]

```

```

RP STRUCTURE BY NMR OF 134-150.
RX MEDLINE=94079874; PubMed=8257679;
RA McInnes C., Soenichsen F.D., Kay C.M., Hodges R.S., Sykes B.D.;
RT "NMR solution structure and flexibility of a peptide antigen
representing the receptor binding domain of Pseudomonas aeruginosa.";
RL Biochemistry 32:13432-13440(1993).
CC -1- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
CC NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
CC CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
CC CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.
CC -1- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M14849; AAA25955.1; -
DR EMBL; X02402; CAA26248.1; -
DR EMBL; S67807; CAB32859.1; -
DR PIR; A03497; YOPSPA.
DR PIR; A24603; A24603.
DR PIR; A28780; A28780.
DR PDB; 1PAJ; 31-JAN-94.
DR PDB; 1PAK; 31-JAN-94.
DR PDB; 1N1L; 29-JAN-96.
DR PDB; 1N1M; 29-JAN-96.
DR InterPro: IPR001082; Piliin.
DR InterPro: IPR001120; Prok_N_methyltn.
DR Pfam: PF00114; Piliin; 1.
DR ProDom: PD000666; Piliin; 1.
DR ProSITE: PS00409; PROKAR_NTER_METHYL; 1.
KW Fimbria; Methylation; 3D-structure.
FT PROPER 1 6
FT CHAIN 7 150 FIMBRIAL PROTEIN.
FT MOD_RES 7 7 METHYLATION (BY SIMILARITY).
FT DISULFID 135 148
FT CONFLICT 90 90 T -> TS (IN REF. 3).
FT CONFLICT 101 103 TAD -> DTA (IN REF. 3).
FT CONFLICT 128 128 A -> D (IN REF. 4).
FT CONFLICT 150 150 R -> K (IN REF. 2).
SO SEQUENCE 150 AA; 15650 MW; COE35869DFD6BE84 CRC64;

Query Match 47.5%; Score 290.5; DB 1; Length 150;
Best Local Similarity 57.8%; Pred. No. 1.4e-19;
Matches 67; Conservative 11; Mismatches 31; Indels 7; Gaps 4;

QY 8 ARSEGASALATINPLKTTVEESLSRGISGKIKIGTTASTAT--ETVAGVDPANKLGIV 65
Db 35 ARSEGASALASVPLKTTVEEALSRSQWS---VKSGTGEDARKKEVPLGVADANKLGIT 91

QY 66 AVAIEDS-GAGDITFTTQGTSSPKNATKVTTLNRT-ADGWACKSTODPMFTPKG 119
Db 92 ALKPPADGTADITLTFWVGAGPKNKKKIITLFTADGLKCKTSDQDEGTFIPKG 147

RESULT 5
FMI_MORBO
ID FMI_MORBO STANDARD; PRT; 159 AA.
AC P20657;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE FIMBRIAL PROTEIN I PRECURSOR (ALPHA PILIN) (I PILIN).
OS Moraxella bovis.
OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae; Moraxella.
OX NCBI_TaxID=476;
RN [1]
RP SEQUENCE FROM N.A.

```

RC STRAIN-PPE63;
 RX MEDLINE-90094235; PubMed=2403542;
 RA Fuls R.A., Maris C.F., Stevens S.P., Green M.R.;
 RT "Sequence analysis of the inversion region containing the pilin genes
 of *Moraxella bovis*.";
 RL J. Bacteriol. 172:310-316(1990).
 RN [2]
 RP SEQUENCE OF 7-159.
 RX MEDLINE-89010522; PubMed=2902184;
 RA Ruehl W.W., Maris C.F., Fernandez R., Falkow S., Schoolnik G.K.;
 RT "Purification, characterization, and pathogenicity of *Moraxella bovis*
 pilin";
 RL J. Exp. Med. 168:983-1002(1988).
 RN [1]
 RP SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
 NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
 CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
 CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED FILUS.
 CC -1 MISCELLANEOUS: MORAXELLA BOVIS CAN EXPRESS EITHER A Q OR A I
 PILIN. THE INVERSION OF 2 KB OF DNA DETERMINES WHICH PILIN IS
 EXPRESSED.
 CC -1 SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation
 at the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC EMBL: M32345; NOT_ANNOTATED_CDS.
 DR PIR: J10071; J10071.
 DR HSSP: P02974; IAY2.
 DR InterPro: IPR001082; PiliN.
 DR Pfam: PF00114; PiliN; 1.
 DR ProDom: PD000666; PiliN; 1.
 DR ProSITE: PS00409; PROKAR_MTER_METHYL; 1.
 KW Fimbria; Methylation.
 FT PROPEP 1 6 FIMBRIAL PROTEIN 1.
 FT CHAIN 7 159 METHYLATION.
 FT MOD.RES 7 7 K -> KSK (IN REF. 2).
 FT CONFLICT 159 159 K -> KSK (IN REF. 2).
 FT SEQUENCE 159 AA; 16723 MW; 9130E2289C7E79E CRC64;
 SQ
 Query Match 17.7%; Score 108.5; DB 1; Length 159;
 Best Local Similarity 33.6%; Pred. No. 0.0036;
 Matches 38; Conservative 14; Mismatches 38; Indels 23; Gaps 7;
 OY 23 KTTVEESLSRG-----IAGSKIKIGTATATETAGVDPANKIGVAV-AIEDSG 73
 DB 50 KTAVDAALFEKPTVLSSESSSKENIGTSS--ET--STKPSNLMASVELGCFADNG 104
 OY 74 AGDIFTQTGTSSPKNATK-VITLNRADGVYACK-----STDDPFTPKG 119
 DB 105 AGTISATL--GNKANKDIKAVITQERTTGDVWCKIDGSOAKKKEFNFTG 155
 RESULT 6
 FMAH_BACNO STANDARD; PRT; 156 AA.
 ID FMAH_BACNO
 AC P04953;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 01-NOV-1991 (Rel. 20, Last annotation update)
 DE FIMBRIAL PROTEIN PRECURSOR (PILIN) (SEROGROUP H1) (265 ANTIGEN) (TWO
 SUBUNITS PILIN).
 GN FIMA.
 OS Bacteroides nodosus (Dichelobacter nodosus).
 OC Bacteria; Proteobacteria; gamma subdivision; Cardiobacteriaceae;
 OC Dichelobacter.
 CX NCBI_TaxID=870;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SEROGROUP H ISOLATE 265;
 RX MEDLINE-86250599; PubMed=2873127;
 RA Elleman T.C., Hoynes P.A., McKern N.M., Stewart D.J.;
 RT "Nucleotide sequence of the gene encoding the two-subunit pilin of
 Bacteroides nodosus 265";
 RL J. Bacteriol. 167:243-250(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SEROGROUP H1 ISOLATE VCS1215;
 RX MEDLINE-91260440; PubMed=1675419;
 RA Mattick J.S., Anderson B.J., Cox P.T., Dalrymple B.P., Bills M.M.,
 RA Hobbs M., Egerton J.R.;
 RT "Gene sequences and comparison of the fimbrial subunits
 representative of Bacteroides nodosus serotypes A to I: class I and
 class II strains";
 RL Mol. Microbiol. 5:561-573(1991).
 CC -1 SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
 NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
 CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
 CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED FILUS.
 CC -1 MISCELLANEOUS: THE SEQUENCE SHOWN IS THAT OF ISOLATE 265.
 CC -1 SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation
 at the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC EMBL: M13765; AAA23346.1; -;
 DR EMBL: X52390; CAA36619.1; -;
 DR HSSP: P02974; IAY2.
 DR InterPro: IPR001082; PiliN.
 DR Pfam: PF00114; PiliN; 1.
 DR ProDom: PD000666; PiliN; 1.
 DR ProSITE: PS00409; PROKAR_MTER_METHYL; 1.
 KW Fimbria; Methylation.
 FT PROPEP 1 79 PILIN SUBUNIT 1.
 FT CHAIN 8 156 PILIN SUBUNIT 2.
 FT MOD.RES 8 8 METHYLATION.
 FT DISULFID 57 67
 FT VARIANT 141 154
 FT VARIANT 91 91
 FT VARIANT 105 105
 FT VARIANT 156 156
 FT SEQUENCE 156 AA; 16637 MW; 7AB398C25AF9B6A6 CRC64;
 SQ
 Query Match 16.8%; Score 103; DB 1; Length 156;
 Best Local Similarity 25.0%; Pred. No. 0.011;
 Matches 30; Conservative 19; Mismatches 61; Indels 10; Gaps 3;
 OY 8 ARSEGSALATINPLKTYVESLSRGIAGSKIKIGTTAS-----TATETAGVPEPA 59
 DB 36 ARSQRVSWSESGQMRATETCLLDKREKDCFGTTSNLLAAGSGTTNATADPQ 95
 OY 60 NKLGIVAVAIEDSGADIFTQTGTSSPKNATKYTLNRTADGVYACKSTDDPFTPKG 119
 DB 96 GGLN-ITVALSEVAENKIEATFGQNAATLHOKK-LITWRSPEARWCSVDDEKFKPTG 153
 RESULT 7
 FMI2_PSEAE STANDARD; PRT; 154 AA.
 ID FMI2_PSEAE
 AC P18774;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE FIMBRIAL PROTEIN PRECURSOR (PILIN) (STRAIN 1244).
 GN PILA OR FIMA.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 CC Pseudomonas.
 ON NCBI_TaxID=287;
 RX [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=89281493; PubMed=2499765;
 RA Castrix P.A., Sidberry H.F., Sadoff J.C.;
 RT "Cloning and sequencing of the Pseudomonas aeruginosa 1244 pilin
 structural gene";
 RL Mol. Gen. Genet. 216:75-80(1989).
 CC -1- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
 CC NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
 CC CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
 CC CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.
 CC -1- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X83916; CAA58768.1; -;
 DR PIR; S04440; S04440.
 DR HSSP; P02974; IAY2.
 DR InterPro: IPR001082; PiliN.
 DR InterPro: IPR001120; Prok_N_methyltn.
 DR Pfam; PF00114; PiliN; 1.
 DR ProDom; PD000666; PiliN; 1.
 DR PROSITE; PS00409; PROKAR_NTER_METHYL; 1.
 KW Fimbria; Methylation.
 FT PROPEP 1 6
 FT CHAIN 7 154 FIMBRIAL PROTEIN.
 FT MOD_RES 7 7 METHYLATION (BY SIMILARITY).
 FT DISULFD 133 151 BY SIMILARITY.
 SO SEQUENCE 154 AA; 16277 MW; 9A6E09E0A6C66ADO CRC64;

Query Match 16.7%; Score 102.5; DB 1; Length 154;
 Best Local Similarity 30.2%; Pred. No. 0.012;
 Matches 35; Conservative 18; Mismatches 42; Indels 21; Gaps 5;

OY 8 ARSEBASALATINPLKTIVEESLSRG--IAGS-----KIKIGTASTATEYVAGVEEDA 59
 DB 35 ARTQYTRAVSEVSALKTAESAILEGKELVSSATPKDYDYGFEESTILD----- 85
 OY 60 NKLGVIAVAIEDSGADITFTFOTGTSPKNA TK--VITLNTFAGVWACKSTOPP 113
 DB 86 -GSGKSQIQVDMNGGTVELVATLKSS-GSAIKGAVITVSKRNDGVNMCKITKTP 139

RESULT 8
 FMKL_PSEAE STANDARD: PRT; 154 AA.
 AC P17836;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE FIMBRIAL PROTEIN PRECURSOR (PILIN) (STRAIN K122-4).
 GN PILA OR FIMA.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 CC Pseudomonas.
 ON NCBI_TaxID=287;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K122-4;

RX MEDLINE=88298689; PubMed=2841299;
 RA Pastosko B.L., Sastry P.A., Finlay B.B., Paranchych W.;
 RT "Two unusual pilin sequences from different isolates of Pseudomonas
 aeruginosa";
 RL J. Bacteriol. 170:3738-3741(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=9D2;
 RX MEDLINE=94131566; PubMed=7507890;
 RA Castrix P.A., Deal C.D.;
 RT "Differentiation of Pseudomonas aeruginosa pilI based on sequence and
 RT B-cell epitope analyses";
 RL Infect. Immun. 62:371-376(1994).
 CC -1- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
 CC NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
 CC CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
 CC CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.
 CC -1- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M21652; AAC63060.1; -;
 DR EMBL; S68100; AAC60460.1; -;
 DR PIR; B31105; B31105.
 DR HSSP; P02974; IAY2.
 DR InterPro: IPR001082; PiliN.
 DR InterPro: IPR001120; Prok_N_methyltn.
 DR Pfam; PF00114; PiliN; 1.
 DR ProDom; PD000666; PiliN; 1.
 DR PROSITE; PS00409; PROKAR_NTER_METHYL; 1.
 KW Fimbria; Methylation.
 FT PROPEP 1 6
 FT CHAIN 7 154 FIMBRIAL PROTEIN.
 FT MOD_RES 7 7 METHYLATION (BY SIMILARITY).
 FT DISULFD 133 151 BY SIMILARITY.
 SO SEQUENCE 154 AA; 16278 MW; 807409FABC66ADO CRC64;

Query Match 16.7%; Score 102.5; DB 1; Length 154;
 Best Local Similarity 30.2%; Pred. No. 0.012;
 Matches 35; Conservative 18; Mismatches 42; Indels 21; Gaps 5;

OY 8 ARSEBASALATINPLKTIVEESLSRG--IAGS-----KIKIGTASTATEYVAGVEEDA 59
 DB 35 ARTQYTRAVSEVSALKTAESAILEGKELVSSATPKDYDYGFEESTILD----- 85
 OY 60 NKLGVIAVAIEDSGADITFTFOTGTSPKNA TK--VITLNTFAGVWACKSTOPP 113
 DB 86 -GSGKSQIQVDMNGGTVELVATLKSS-GSAIKGAVITVSKRNDGVNMCKITKTP 139

RESULT 9
 FMAD_BACNO STANDARD: PRT; 156 AA.
 AC P13253;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE FIMBRIAL PROTEIN PRECURSOR (PILIN) (SEROGROUP D) (340 ANTIGEN).
 GN FIMA.
 OS Bacterioides nodosus (Dichelobacter nodosus).
 OC Bacteria; Proteobacteria; gamma subdivision; Cardiobacteriaceae;
 CC Dichelobacter.
 ON NCBI_TaxID=870;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SEROGROUP D ISOLATE VCS1172;

RX MEDLINE-91260440; PubMed-1675419;
 RA Matlick J.S., Anderson B.J., Cox P.T., Dalrymple B.P., Bills M.M.,
 RA Hobbs M., Egerton J.R.,
 RT "Gene sequences and comparison of the fimbrrial subunits
 RT representative of Bacteroides nodosus serotypes A to I: class I and
 RT class II strains."
 RL Mol. Microbiol. 5:561-573(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SEROGROUP D ISOLATE 340;
 RX MEDLINE-89036113; PubMed-9183618;
 RA Finney K.G., Ellemann T.C., Stewart D.J.;
 RT "Nucleotide sequence of the pilin gene of Bacteroides nodosus 340
 RT (serogroup D) and implications for the relatedness of serogroups."
 RL J. Gen. Microbiol. 134:575-584(1988).
 CC -1- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
 CC NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
 CC CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
 CC CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.
 CC -1- MISCELLANEOUS: THE SEQUENCE SHOWN IS THAT OF ISOLATE 340.
 CC -1- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X52389; CAA36618.1; -
 DR EMBL: M20369; AAA23347.1; -
 DR PIR: S15266; S15266.
 DR HSSP: Q53391; 1K88.
 DR InterPro: IPR001082; PiliN.
 DR InterPro: IPR001120; Prok_N_methyltn.
 DR Pfam: PF00114; PiliN; 1.
 DR ProDom: PD000666; PiliN; 1.
 DR PROSITE: PS00409; PROKAR_NTER_METHYL; 1.
 DR Fimbrria; Methylation.
 KW PROPEP 1
 FT CHAIN 8 156 FIMBRIAL PROTEIN.
 FT MOD_RES 8 8 METHYLATION (BY SIMILARITY).
 FT DISULFID 57 67 BY SIMILARITY.
 FT VARIANT 140 153 BY SIMILARITY.
 FT VARIANT 65 66 GE -> DK (IN ISOLATE 340).
 FT VARIANT 80 80 D -> E (IN ISOLATE 340).
 FT VARIANT 95 95 A -> T (IN ISOLATE 340).
 SQ SEQUENCE 156 AA; 16544 MW; 45418C8C22BBE93C CRC64;
 Query Match 16.1%; Score 98.5; DB 1; Length 156;
 Best Local Similarity 26.0%; Pred. No. 0.028;
 Matches 32; Conservative 21; Mismatches 53; Indels 17; Gaps 4;
 Oy 8 ARSEGASALATINPLKTTVESISRGISKIKITASTAT--ETVAGVDPDANKIGVI 65
 Db 36 ARSOVSRYVSETGOMRTAIECTVLDGKPCAGECFIGWTSNLLDGFATGTESTAATGQA 95
 Oy 66 AVAIEDSGA---GDITFTFOTGTSPPKNT---KYITLNRADGVMACKSQDDPFT 116
 Db 96 GITIKYPAADDEGNIVATF-----GNNAALAKIPOTLTWSRSKEGTWCATTVEAKFQ 149
 Oy 117 PKG 119
 Db 150 PTG 152
 RESULT 10
 ID ECPA_EIKCO STANDARD; PRT; 159 AA.
 AC P35645;
 DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE FIMBRIAL PROTEIN ECPA PRECURSOR (PILIN).
 GN ECPA
 OS Eikenella corrodens.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Eikenella.
 OX NCBI_Taxid=539;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 23834;
 RX MEDLINE-9332782; PubMed-8473871;
 RA Rao V.K., Prokuske-Fox A.;
 RT "Cloning and sequencing of two type 4 (N-methylphenylalanine) pilin
 RT genes from Eikenella corrodens."
 RL J. Gen. Microbiol. 139:651-660(1993).
 CC -1- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: Z12609; CAA78250.1; -
 DR PIR: S23844; S23844.
 DR PIR: A47699; A47699.
 DR HSSP: P02974; 1A92.
 DR InterPro: IPR001082; PiliN.
 DR InterPro: IPR001120; Prok_N_methyltn.
 DR Pfam: PF00114; PiliN; 1.
 DR ProDom: PD000666; PiliN; 1.
 DR PROSITE: PS00409; PROKAR_NTER_METHYL; 1.
 DR Fimbrria; Methylation.
 KW PROPEP 1
 FT CHAIN 8 159 POTENTIAL.
 FT MOD_RES 8 8 METHYLATION (BY SIMILARITY).
 FT DISULFID 139 158 BY SIMILARITY.
 SQ SEQUENCE 159 AA; 16177 MW; 7C3D4D9DA9B1B8C2 CRC64;
 Query Match 14.4%; Score 88; DB 1; Length 159;
 Best Local Similarity 28.3%; Pred. No. 0.25;
 Matches 30; Conservative 14; Mismatches 54; Indels 8; Gaps 3;
 Oy 8 ARSEGASALATINPLKTTVESISRG---IAGSKIKIGTASTATETVAGVDPDANKIGV 64
 Db 36 SKSOVTRAYGEMAGTKTAIEALFEGRTPVLAATAAGAAATPPNENWGMIDNPISNLS 95
 Oy 65 IAVAIEDSGADITFTFOTG---TSSPKNTKYITLNRADGVMACKSQDDPFT 107
 Db 96 AATLTGPNAGADVTEVGTIGENANNSIHGAT--ITLTCTASGHWTC 139
 RESULT 11
 ID KDC2_DROME
 AC KDC2_DROME STANDARD; PRT; 502 AA.
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE PROTEIN KINASE DC2 (EC 2.7.1.1-).
 GN DC2 OR PKA-C3.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_Taxid=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CANTON-S;
 RX MEDLINE-89107990; PubMed=3215511;

RA Kalderson D., Rubin G.M.;
 RT "Isolation and characterization of Drosophila cAMP-dependent protein
 kinase genes.";
 RL Genes Dev. 2:1539-1556(1988).
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN = ADP + A PHOSPHOPROTEIN.
 CC -1- TISSUE SPECIFICITY: MORE ABUNDANT IN ADULT HEAD THAN ADULT BODY.
 CC -1- DEVELOPMENTAL STAGE: IN EMBRYONS, PUPAE AND ADULTS.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC CAMP SUBFAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X16961; CAA34835.1; -
 DR PIR: F31751; F31751.
 DR HSSP: P05132; 2CPK.
 DR FlyBase: FBgn0000489; Pka-C3.
 DR InterPro: IPR000719; Euk.pkinase.
 DR InterPro: IPR002290; Ser_thr_kin_actsite.
 DR Pfam: PF00069; Pkinase.1.
 DR Pfam: PF00433; Pkinase.C; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR SMART: SM00133; S_TK_X; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR Trnsterase: Serine/threonine-protein kinase; ATP-binding.
 FT DOMAIN 193 447 PROTEIN KINASE.
 FT NP_BIND 199 207 ATP (BY SIMILARITY).
 FT BINDING 222 222 ATP (BY SIMILARITY).
 FT ACT_SITE 316 316 BY SIMILARITY.
 SO SEQUENCE 502 AA; 56960 MW; CAA474A5A40193D CRC64;

Query Match 13.8%; Score 84.5; DB 1; Length 502;
 Best Local Similarity 29.9%; Pred. No. 1.8;
 Matches 26; Conservative 18; Mismatches 34; Indels 9; Gaps 3;

OY 30 LSRGAGSKIRIGT--TASTATETTYAGVEDANKGVIAVAIEDSGAGDITFTFGTGS 86
 DB 13 LSSGAGSTSKLTGNGSGNMTSAKKRIPSNN-----STANDSNTETTFEKLGRS 67
 OY 87 SPKNATKYITLRRADGWACKSTODP 113
 DB 68 NGRSSSNVAS-SESSDPLESDSEEDP 93

RESULT 12
 ID FLIC_ECOLI STANDARD: PRT: 497 AA.
 AC P04949;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE FLAGELLIN
 GN FLIC OR PLAF OR HAG OR B1923.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12;
 RX MEDLINE=87057066; PubMed=3536885;
 RA Kuwajima G., Asaka J.-I., Fujiwara T., Fujiwara T., Node K., Kondo E.;
 RT "Nucleotide sequence of the hag gene encoding flagellin of
 Escherichia coli.";

RL J. Bacteriol. 168:1479-1483(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12;
 RX MEDLINE=89281489; PubMed=2659972;
 RA Hanafusa T., Sakai A., Tomioka A., Enomoto M.;
 RT "Isolation and characterization of Escherichia coli hag operator
 mutants whose hag48 expression has become repressible by a Salmonella
 RT HI repressor.";
 RL Mol. Gen. Genet. 216:44-50(1989).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12; MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blatter F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1232-1244(1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12;
 RX MEDLINE=97251358; PubMed=9097040;
 RA Itoh T., Alba H., Baba T., Fujita K., Hayashi K., Inada T.,
 RA Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,
 RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
 RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T.,
 RA Saito N., Sampei G., Seki Y., Sivasubramanian S., Tagami H.,
 RA Takeda J., Takemoto K., Mada C., Yamamoto Y., Horikuchi T.;
 RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
 RT corresponding to the 40.1-50.0 min region on the linkage map.";
 RL DNA Res. 3:379-392(1996).
 RN [5]
 RP SEQUENCE OF 1-19 FROM N.A.
 RX MEDLINE=8338225; PubMed=6305924;
 RA Szekely E., Simon M.;
 RT "DNA sequence adjacent to flagellar genes and evolution of flagellar-
 RT phase variation.";
 RL J. Bacteriol. 155:74-81(1983).
 RN [6]
 RP SEQUENCE OF 1-12.
 RC STRAIN-K12 / EMG2;
 RX MEDLINE=97443975; PubMed=9298646;
 RA Link A.J., Robison K., Church G.M.;
 RT "Comparing the predicted and observed properties of proteins encoded
 RT in the genome of Escherichia coli K-12.";
 RL Electrophoresis 18:1259-1313(1997).
 CC -1- FUNCTION: FLAGELLIN IS THE SUBUNIT PROTEIN WHICH POLYMERIZES TO
 CC FORM THE FILAMENTS OF BACTERIAL FLAGELLA.
 CC -1- SIMILARITY: BELONGS TO THE BACTERIAL FLAGELLIN FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M14358; AAA23950.1; -
 DR EMBL: X17440; CAA35488.1; -
 DR EMBL: AE000285; AAC74990.1; -
 DR EMBL: D90832; BA15744.1; -
 DR EMBL: D90833; BA15751.1; -
 DR EMBL: J01607; AAA92491.1; -
 DR PIR: A37249; FLEC.
 DR SWISS-2DPAGE: P04949; COLI.
 DR Ecogene: EG10321; FLIC.
 DR InterPro: IPR001029; Flagellin_C.
 DR InterPro: IPR001492; Flagellin_N.
 DR Pfam: PF00669; Flagellin_C; 1.
 DR Pfam: PF00669; Flagellin_N; 1.

DR PRINTS: PR00207; FLAGELLIN.
 DR PRODOM: PD000316; Flagellin_C. 1.
 KW Flagella: Complete proteome.
 FT INIT MET 0
 FT CONFLICT 284 284
 SO SEQUENCE 497 AA; 51163 MW; 24B5419C21C7B4E8 CRC64.

Query Match
 Best Local Similarity 13.2%; Score 80.5; DB 1; Length 497;
 Matches 31; Conservative 17; Mismatches 34; Indels 41; Gaps 4;

OY 1 ALEGTFFANSEASALATINPLKTTVESLSRGIASKIKIGTASTATETIYACVEPDAN 60
 DB 250 ANDGT-VTATGATATANATVTDANTTKATTITSG--GTVOVDNTRAGSAT-----AN 297
 OY 61 KIGVIAVAIEDSGAGD-----TFFPOTGTSSPKNA 91
 DB 298 LGAVSLVTKIDSKNDTDTYALKDTNGMLYADVNETTGAVSVKTIYTTDSSGAASSPTA 357
 OY 92 TKV 94
 DB 358 VKL 360

RESULT 13
 FMWC_PSEPU STANDARD; PRT; 136 AA.
 AC P36643;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE FIMBRIAL PROTEIN PRECURSOR (PILIN).
 GN PILA.
 OS Pseudomonas putida.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OX NCBI_TaxID=103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MCS358;
 RX MEDLINE-94131942; PubMed-7905475;
 RA de Groot A., Heijnen I., de Cock H., Filloux A., Tommassen J.;
 RT "Characterization of type IV pilus genes in plant growth-promoting
 RL Pseudomonas putida MCS358".
 CC J. Bacteriol. 176:642-650(1994).
 CC -1- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC at the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X74276; CAAS2332.1;
 DR PIR: S35951; S35951.
 DR HSSP: P02974; IAY2.
 DR InterPro: IPR001082; PiliN.
 DR InterPro: IPR001120; Prok_N_methyltn.
 DR Pfam: PF00114; PiliN; 1.
 DR PRODOM: PD000666; PiliN; 1.
 DR PROSITE: PS00409; PROKAR_NTER_METHYL; 1.
 KW Fimbria; Methylation.
 FT PROPEP 1 6
 FT CHAIN 7 136
 FT MOD_RES 7 7
 FT DISULFID 120 133
 SO SEQUENCE 136 AA; 13632 MW; B3C3BB3333E5D5CF CRC64;

Query Match 13.1%; Score 80; DB 1; Length 136;

Best Local Similarity 24.8%; Pred. No. 1.1;
 Matches 28; Conservative 16; Mismatches 53; Indels 16; Gaps 4;

OY 8 ARSEGASALATINPLKTTVESLSRGIASKIKIGTASTATETIYACVEPDANKGVIAV 67
 DB 35 SRTKAAAGLEISALKTAMDRLNKG-----KDVAVGALGGQPAFAHCAITAS 83
 OY 68 AIEDSGAGDITFTFFGTGTSSPKNAT-KVITLNRATDGVACSTODPMFTPKG 119
 DB 84 GNAAGGIVCTL---VDAPATVVGKALTLRSATG-WCCTTNIIEEDLABSG 132

RESULT 14
 FMAE_BACNO STANDARD; PRT; 161 AA.
 AC P17925;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 01-AUG-1990 (Rel. 23, Last annotation update)
 DE FIMBRIAL PROTEIN PRECURSOR (PILIN) (SEROGROUP E2).
 GN FIMA.
 OS Bacteroides nodosus (Dichelobacter nodosus).
 OC Bacteria; Proteobacteria; gamma subdivision; Cardiobacteriaceae;
 OC Dichelobacter.
 OX NCBI_TaxID=870;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SEROGROUP E2 ISOLATE VCS1114;
 RX MEDLINE-91260440; PubMed-1675419;
 RA Mattick J.S., Anderson B.J., Cox P.T., Dalrymple B.P., Bills M.M.,
 RA Hobbs M., Egerton J.R.;
 RT "Gene sequences and comparison of the fimbrial subunits
 RT representative of Bacteroides nodosus serotypes A to I: class I and
 RL Mol. Microbiol. 5:561-573(1991).
 CC -1- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
 CC NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
 CC CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
 CC CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.
 CC -1- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
 CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC at the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL: X52407; CAA36656.1;
 DR PIR: S15262; S15262.
 DR HSSP: Q53391; 1K88.
 DR InterPro: IPR001082; PiliN.
 DR InterPro: IPR001120; Prok_N_methyltn.
 DR Pfam: PF00114; PiliN; 1.
 DR PRODOM: PD000666; PiliN; 1.
 DR PROSITE: PS00409; PROKAR_NTER_METHYL; 1.
 KW Fimbria; Methylation.
 FT PROPEP 1 7
 FT CHAIN 8 161
 FT MOD_RES 8 8
 FT DISULFID 8 8
 SO SEQUENCE 161 AA; 16812 MW; B7EB577906E73BE CRC64;

Query Match 12.7%; Score 77.5; DB 1; Length 161;
 Best Local Similarity 28.3%; Pred. No. 2.2;
 Matches 36; Conservative 13; Mismatches 53; Indels 25; Gaps 6;

OY 8 ARSEGASALATINPLKTTVESLSRGI-----AGSKIKIGTASTATE---TYAGVE 56
 DB 36 ARSQAAEGITLADGLKIRIDHLENGCTEDANAGAGCKGNDTGKYYALAEIGGTVA--- 92
 OY 57 PDANKGVIAVAIEDSGAGDITFTFFGTGTSSPKNA-----TKVITLNRATDGVW--ACKST 110

DB 93 ODATNL-----KPEDNCTVTITTYGKAGAKISKLLDFTKLELDQLVNGSYTGCAFT 147
 OY 111 ODPMPFP 117
 DB 148 LDAKFP 154

RESULT 15

ID HP12_DEIRA STANDARD: PRF, 1036 AA.
 AC P13126:

DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE HEXAGONALLY PACKED INTERMEDIATE-LAYER SURFACE PROTEIN PRECURSOR.
 GN HPI.

OS Deinococcus radiodurans.

OC Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.

OX NCBI_taxid=1293;

RN (1)
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC STRAIN-SARK;

RX MEDLINE-88032846; PubMed-3667529:

RA Peters J., Peters M., Lottspeich F., Schaefer W., Baumeister W.:
 "Nucleotide sequence analysis of the gene encoding the Deinococcus

radiodurans surface protein, derived amino acid sequence, and
 complementary protein chemical studies."

RT J. Bacteriol. 169:5216-5223(1987).

RL -1- FUNCTION: SHAPE MAINTENANCE, POSSIBLE PROTECTION FROM NOXIOUS
 ENZYMES OR EXOGENOUS AND UNSETTLING DNA, AND MAY MEDIATE HOMOTYPIC

CELL-CELL CONTACTS.

CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
 HEXAGONAL S-LAYER.

CC -1- PTM: CONTAINS TIGHTLY BOUND REDUCING SUGARS (SIX PER POLYPEPTIDE
 CHAIN) AND FATTY ACIDS (COVALENTLY BOUND AND LOCATED IN THE N-

CC -1- PTM: THE N-TERMINUS IS BLOCKED.

CC -1- MISCELLANEOUS: THE HYDROPHILIC C-TERMINAL REGION RICH IN AROMATIC
 AA COULD BE ENGAGED IN INTERACTIONS WITH NUCLEIC ACIDS, AND THE

CC BOUND FATTY ACIDS AND THE N-TERMINAL REGION COULD SERVE TO ANCHOR
 THE LAYER TO THE OUTER MEMBRANE OF D. RADIODURANS. HPI LAYER

CC CONTAIN ABOUT 30% BETA STRUCTURE AND VIRTUALLY NO ALPHA HELIX.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@sib-sib.ch).

CC -----

CC EMBL, M17895; AAA23335.1; -

CC DR PIR: A29832; A29832.

CC DR HSSP: P11795; 2TBV.

CC DR PROSITE: PS00013; PROKAR_LIPOPROTEIN; UNKNOWN_1.

CC KW Glycoprotein; Lipoprotein; Signal; Cell wall; S-layer.

CC FT SIGNAL 1 17 POTENTIAL.

CC FT CHAIN 18 1036 HEXAGONALLY PACKED INTERMEDIATE-LAYER

CC FT DISULFID 74 86 SURFACE PROTEIN.

CC FT DISULFID 256 275 PROBABLE.

CC FT DISULFID 642 754

CC FT DOMAIN 60 250 SER/THR-RICH (29%).

CC FT DOMAIN 985 1030 RICH IN AROMATIC AA (29%).

CC FT SEQUENCE 1036 AA; 108028 MW; AAF98206A74AEE CRC64;

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

Search completed: February 8, 2002, 15:34:22
 Job time: 547 sec

DB 109 TDAARNVGTSSVAVTVNACVSNPAPTAVLTIDLAGVSSAPITIKDANGNVVGGYDNTV 168
 OY 58 DANKLGVIYVAIEDSGAGDI-----TFPFGTSSPKNATVITLNRADGVMAACKSTQ 111
 DB 169 NDMATITVARGVYTVTAGVSGFNGFTNFRDLS-----GNGTYTLNTQAG-----TT 219
 OY 112 DPMFTPKGSDN 122
 DB 220 TP--TPVGSIN 228

OY 5 TEFARSEGASALATI-----NPLKTTVESLS-RGIAGSKIRIGTASTATETVAGVEP 57

Query Match 12.6%; Score 77; DB 1; Length 1036;
 Best Local Similarity 25.2%; Pred. No. 19;
 Matches 33; Conservative 20; Mismatches 54; Indels 24; Gaps 6;

Fri Feb 8 15:44:54 2002

us-09-865-159-6.rsp

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 8, 2002, 15:33:53 ; Search time 67.44 Seconds

(without alignments)
264.609 Million cell updates/sec

Title: US-09-865-159-6

Sequence: 1 ALEGTFAFASGASALATIN.....GWACKSTODPMTPKGSDN 122

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_17:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.prodent:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	398	65.0	150	2	059795
2	135.5	22.1	139	2	092EL3
3	116.5	19.0	148	2	09PAH6
4	114	18.6	153	2	09X4G7
5	113	18.5	167	2	09KPE5
6	112	18.3	140	2	09E671
7	112	18.3	146	2	052613
8	107	17.5	130	2	09S4E2
9	107	17.5	136	2	056799
10	105.5	17.2	131	2	09AP36
11	105.5	17.2	157	2	059336
12	102.5	16.7	159	2	059505
13	102	16.7	145	2	09APK5
14	102	16.7	148	2	09PAH9
15	100.5	16.4	154	2	059794
16	100	16.3	135	2	056800
17	90.5	14.8	147	2	030583
18	90	14.7	116	2	09APJ3
19	87.5	14.3	158	2	059508

20	86	14.1	540	9	09G0H8	09G0H8 roseophage
21	84	13.7	595	2	006351	006351 escherichia
22	84	13.7	595	2	09S0U1	09S0U1 escherichia
23	83	13.6	160	2	059504	059504 moraxella b
24	83	13.6	397	5	09V581	09V581 drosophila
25	82.5	13.5	568	2	09S0T5	09S0T5 escherichia
26	82	13.4	130	2	09APJ4	09APJ4 xanthomonas
27	82	13.4	158	2	054650	054650 bacteroides
28	82	13.4	158	2	059501	059501 moraxella b
29	82	13.4	1042	5	09V2A9	09V2A9 drosophila
30	80.5	13.2	159	2	060163	060163 moraxella b
31	79.5	13.0	496	2	09CK07	09CK07 schistosach
32	79.5	13.0	1220	3	09C0Y2	09C0Y2 schistosach
33	79	12.9	217	2	09X6X0	09X6X0 streptococc
34	79	12.9	588	5	09VG48	09VG48 drosophila
35	78.5	12.8	568	2	053789	053789 shigella bo
36	77.5	12.7	233	5	09VUV5	09VUV5 drosophila
37	76.5	12.5	398	2	09MMR6	09MMR6 pseudomonas
38	76.5	12.5	638	2	0918K5	0918K5 mycobacteri
39	76.5	12.5	2625	3	09C238	09C238 neurospora
40	76.5	12.5	3309	5	09VML2	09VML2 drosophila
41	76	12.4	337	5	09W4M1	09W4M1 drosophila
42	75.5	12.3	134	2	09S4E1	09S4E1 bacteroides
43	75.5	12.3	156	2	059507	059507 moraxella b
44	75.5	12.3	252	1	09Y984	09Y984 aeropyrum p
45	75.5	12.3	273	2	09Z680	09Z680 borrelia sp

ALIGNMENTS

RESULT 1
ID 059795 PRELIMINARY: PRT: 150 AA.
AC 059795;
DT 01-JUN-1998 (TREMREL. 06, Created)
DT 01-JUN-1998 (TREMREL. 06, Last sequence update)
DT 01-JUN-2001 (TREMREL. 17, Last annotation update)
DE FILIAL PROTEIN PRECURSOR (PILIN) (STRAIN T2A).
GN PILA OR FILA.
OS Pseudomonas aeruginosa.
OC Bacteria: Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_Taxid=287;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-T2A.
RX MEDLINE-94131566; PubMed-7507890;
RA Gastric P.A. Deal C.D.;
RT "Differentiation of Pseudomonas aeruginosa pil based on sequence and
RT B-cell epitope analyses."
RL Infect. Immun. 62:371-376(1994).
CC -I- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
CC NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
CC CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
CC CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.
CC -I- SIMILARITY: BELONGS TO THE N-W-PHE PILI FAMILY.
CC EMBL: S68102; AAC60462.1; -
DR HSSP: P02973; INIL.
DR InterPro: IPR001082; PiliN.
DR Pfam: PF00114; PiliN.1.
DR ProDom: PD000666; PiliN.1.
DR PROSITE: PS00409; PROKAR_NTER_METHYL.1.
KW Fimbria; Methylation.
FT PROPEP 1 6 FIMBRIAL PROTEIN.
FT CHAIN 7 150 BY SIMILARITY.
FT DISULFD 134 147 METHYLATION (BY SIMILARITY).
FT MOD_RES 7 7
SQ SEQUENCE 150 AA; 15356 MW; A/F21CD92AF3DCFI CRC64;
Query Match 65.0%; Score 398; DB 2; Length 150;

Best Local Similarity 72.3%; Pred. No. 1.7e-27;
Matches 81; Conservative 7; Mismatches 24; Indels 0; Gaps 0;

QY 8 ASSEGASALATINPLKTYVESLSRGISGKIKIGTASTATETAGYVPEPANKLGIVAV 67
DB 35 ASSEGASALATINPLKTYVESLSRGISGKIKIGTASTATETAGYVPEPANKLGIVAV 94
QY 68 AIEDSGAGDITFTFOTGSSPKNATKVTITNRTADGVWACKSTODPMFTPG 119
DB 95 TIGNNAGTIVTTPFAAGNSPRKSGAIIITRTDAGSWACKSTODEMFTPG 146

RESULT 2

Q9ZEL3 PRELIMINARY; PRT: 139 AA.
ID Q9ZEL3
AC Q9ZEL3
DT 01-MAY-1999 (TREMblrel. 10, Created)
DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE TYPE IV PILIN SUBUNIT.
GN PILA OR PILAI.
OS Pseudomonas stutzeri (Pseudomonas perfectomarina).
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OX Pseudomonas.
NCBI_TaxID=316;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-JM300;
RA Graupner S., Lorenz M.G., Wackernagel W.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-JM300;
RA Graupner S., Wackernagel W.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
CC NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
CC CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
CC CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS (BY
CC SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE FIMBRIAL PROTEIN (N-ME-PHE)PILIN
CC FAMILY.
DR EMBL: AJ132364; CAI0652.1;
DR EMBL: AJ249743; CAB60734.1;
DR InterPro: IPR002416; Bac_GSPH.
DR InterPro: IPR001082; Pilin.
DR InterPro: IPR001120; Prok_N_methyltn.
DR Pfam: PF00114; pilin; 1.
DR PRINTS: PR00885; BCTERIALGSPH.
DR PRODOM: PD000666; pilin; 1.
DR PROSITE: PS00409; PROKAR_NTER_METHYL. 1.
DR FIMBRIA: Methylation.
KW MOD. RES.
FT MOD. RES.
SQ SEQUENCE 139 AA; 14558 MW; C3C0DCEFOA9EA770 CRC64;

Query Match 22.1%; Score 135.5; DB 2; Length 139;
Best Local Similarity 36.0%; Pred. No. 0.00012;
Matches 41; Conservative 10; Mismatches 42; Indels 21; Gaps 3;

QY 9 RSEGASALATINPLKTYVESLSRGISGKIKIGTASTATETAGYVPEPANKLG 63
DB 38 RSNAAALAEITPGKIGFEOAINESKTPSLSTDEGTYGIDTST--SYCDVDLDTADG 94
QY 64 VIVAAIESGAGDITFTFOTGSSPKNATKVTITNRTADGVWACKSTODPMFTPG 117
DB 95 HIECTAKGNAG-----KFDGKTIITNRTADGEMSCASTLDKAKYK 135

RESULT 3
Q9PAH6 PRELIMINARY; PRT: 148 AA.
ID Q9PAH6
AC Q9PAH6

DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE FIMBRIAL PROTEIN.
GN Xf2542.
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC Xylella.
NCBI_TaxID=2371;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-9A5C;
RX MEDLINE=20365717; PubMed=10910347;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Bata G.S., Baptista C.S.,
RA Barros M.R., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carier H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frome M., Furian L.R.,
RA Garlier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hohnselt J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Kriesger J.E., Kuzamae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.T.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhani A., Jr., Nodrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A., Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA da Rosa V.E., Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A., Jr.,
RA de Souza A.P., Terezzi M.F., Siqueira M.L.Z., Siqueira W.D., de Souza A.A.,
RA Vallada H., Van Slyks M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa.";
RL Nature 406:151-159(2000).

CC -1- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
CC NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
CC CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
CC CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS (BY
CC SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE FIMBRIAL PROTEIN (N-ME-PHE)PILIN
CC FAMILY.
DR EMBL: AE004061; AAF85339.1;
DR InterPro: IPR002416; Bac_GSPH.
DR InterPro: IPR001082; Pilin.
DR InterPro: IPR001120; Prok_N_methyltn.
DR Pfam: PF00114; pilin; 1.
DR PRINTS: PR00885; BCTERIALGSPH.
DR PRODOM: PD000666; pilin; 1.
DR PROSITE: PS00409; PROKAR_NTER_METHYL. 1.
DR COMPLETE PROTEOME: Fimbria; Methylation.
KW SEQUENCE 148 AA; 15034 MW; F17C024F2716EDD5 CRC64;

Query Match 19.0%; Score 116.5; DB 2; Length 148;
Best Local Similarity 32.5%; Pred. No. 0.0058;
Matches 40; Conservative 8; Mismatches 50; Indels 25; Gaps 4;

QY 8 ASSEGASALATINPLKTYVESLSRGISGKIKIGTASTATETAGYVPEPANKLGIVAV 67
DB 35 ASQAALAEITPGKIGFEOAINESKTPSLSTDEGTYGIDTST--SYCDVDLDTADG 94
QY 68 AIEDSGAGDITFTFOTGSSPKNATKVTITNRTADGVWACKSTODPMFTPG 116
DB 84 DIAPSAASAITCT-WIGNAQNNT--ITLRIADNNAAGGCVNTGWMCTTTAPALIT 140
QY 117 PKG 119

AC Q9KPE5; 2000 (Tremblref. 15, Created)
 DT 01-OCT-2000 (Tremblref. 15, Last sequence update)
 DT 01-OCT-2000 (Tremblref. 15, Last sequence update)
 DT 01-JUN-2001 (Tremblref. 17, Last annotation update)
 DE FIMBRIAL PROTEIN.
 GN VC2423.
 OS *Vibrio cholerae*.
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; *Vibrio*

RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=WCS365;
RA Caracho Carvajal M.M., de Priester W., Luftenberg B.J.J.

RA Bloembergen G.V.;
RT "Involvement of type 4 pilli of *Pseudomonas fluorescens* in tomato root

RT colonization.";
 RL Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases
 CC -1- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
 CC NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
 CC CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
 CC CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE FIMBRIAL PROTEIN (N-ME-PHE)PILIN
 CC FAMILY.
 DR EMBL: AF297457; AAC18586.1; -
 DR Interpro: IPR002416; Bac_GSPH.
 DR Interpro: IPR001082; Piliin.
 DR Interpro: IPR001120; Prok_N_methyltn.
 DR Pfam: PF00114; Piliin; 1.
 DR PRINTS: PR00885; BCTERIALGSPH.
 DR PRODOM: PD000666; Piliin; 1.
 DR PROSITE: PS00409; PROKAR_NTER_METHYL; 1.
 DR Fimbrin; Methylation.
 KW Fimbrin; Methylation.
 SQ SEQUENCE 140 AA; 14077 MW; 3299B0751C6603C4 CRC64;

Query Match 18.5%; Score 113; DB 2; Length 140;
 Best Local Similarity 32.5%; Pred. No. 0.011;
 Matches 38; Conservative 13; Mismatches 42; Indels 24; Gaps 4;

OY 8 ARSEGASALATINPLKTTVEESLSRGISGSKIKIGTTASTATETVAGVEPDANKLGIVAV 67
 DB 35 ARAKVYGLAEASLSKYPVEDLNKG-----TSPTAANT--GVASSNCTM--- 79
 OY 68 AIEDSGAGDITTFQGTSSPKNAT-----KVTLNRTADGVACKSTODPMETPKG 119
 DB 80 ----SVSGDATAGTATVTAIKKAPSSIVGKTTTISRAGTGWSCSNVAEEFLPAG 132
 RESULT 7
 ID 052613 PRELIMINARY; PRT; 146 AA.
 AC 052613
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE FIMBRILIN.
 GN FIMA.
 OS Xanthomonas campestris (pv. citri).
 OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
 OC Xanthomonas.
 OX NCBI_TaxID=346;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-XM47;
 RA Kuo T.T., Su W.C.;
 RL Submitted (Jan-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
 CC NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
 CC CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
 CC CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE FIMBRIAL PROTEIN (N-ME-PHE)PILIN
 CC FAMILY.
 DR EMBL: AF042829; AAB97527.1; -
 DR Interpro: IPR001082; Piliin.
 DR Interpro: IPR001120; Prok_N_methyltn.
 DR Pfam: PF00114; Piliin; 1.
 DR PRODOM: PD000666; Piliin; 1.
 DR PROSITE: PS00409; PROKAR_NTER_METHYL; 1.
 DR Fimbrin; Methylation.
 KW Fimbrin; Methylation.
 SQ SEQUENCE 146 AA; 15249 MW; 6D0C7F3CEB24DAE CRC64;

Query Match 18.3%; Score 112; DB 2; Length 146;
 Best Local Similarity 32.0%; Pred. No. 0.014;
 Matches 33; Conservative 13; Mismatches 49; Indels 8; Gaps 2;

OY 8 ARSEGASALATINPLKTTVEESLSRGISGSKIKIGTTASTATETVAGVEPDANKLGIVAV 67
 DB 35 ARAKVYGLAEASLSKYPVEDLNKG-----KGTTLTAAVGLGATSTNNRSATIV 87
 OY 68 AIEDSGAGDITTFQGTSSPKNATKVTLNRTADGVACKSTODPMETPKG 109
 DB 88 LAPDATAGBOTNALSCITLGSAPRIVGKITWARDINGWTCST 130

RESULT 8
 ID 09S4E2 PRELIMINARY; PRT; 130 AA.
 AC 09S4E2;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE FIMBRIL SUBUNIT (FRAGMENT).
 GN FIMA.
 OS Bacteroides nodosus (Dichelobacter nodosus).
 OC Bacteria; Proteobacteria; gamma subdivision; Cardiobacteriaceae;
 OC Dichelobacter.
 OX NCBI_TaxID=870;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhou H., Hickford J.G.H.;
 RT "Dichelobacter nodosus fimbrial subunit gene (fima).";
 RT Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Zhou H., Hickford J.G.H.;
 RT "Dichelobacter nodosus fimbrial subunit gene.",
 RT Submitted (Oct-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF146890; AAB3087.1; -
 DR EMBL: AF316611; AAK0324.1; -
 DR Interpro: IPR001082; Piliin.
 DR Pfam: PF00114; Piliin; 1.
 DR PRODOM: PD000666; Piliin; 1.
 DR NON_TER 1
 FT SEQUENCE 130 AA; 13838 MW; 097BD2488FEA6C9D CRC64;

Query Match 17.5%; Score 107; DB 2; Length 130;
 Best Local Similarity 25.8%; Pred. No. 0.034;
 Matches 31; Conservative 19; Mismatches 60; Indels 10; Gaps 3;

OY 8 ARSEGASALATINPLKTTVEESLSRGISGSKIKIGTTAS-----TATETVAGVEPDA 59
 DB 10 ARSQVSRVSEFGMRATIECLDGRKDCFIGWTSNLLAAGSTNNATADPCG 69
 OY 60 NKLGVIAVAIEDSGAGDITTFQGTSSPKNATKVTLNRTADGVACKSTODPMETPKG 119
 DB 70 GGLN-IAVALESTAEKNKTEATFGQNAATLHGKK-LTWTRSPBPAWSCSYDVEKFKPTG 127
 RESULT 9
 ID 056799 PRELIMINARY; PRT; 136 AA.
 AC 056799;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE FIMBRILIN.
 GN FIMA.
 OS Xanthomonas campestris.
 OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
 OC Xanthomonas.
 OX NCBI_TaxID=339;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=3240 (NCPB);
 MEDLINE=97175558; PubMed=9023213;
 Ojanen-Reus T., Kalkkinen N., Westerlund-Wikstrom B., van Doorn J.,

RA Hahtela K., Nurmiaho-Lassila E.L., Mengelink K., Bonas U.,
 RA Korhonen T.K.,
 RT "Characterization of the fimA gene encoding bundle-forming fimbriae of
 RT the plant pathogen *Xanthomonas campestris* pv. *vesicatoria*.";
 RL J. Bacteriol. 179:1280-1290(1997).
 DR EMBL: 248759; CAAB8680.1; -
 DR InterPro: IPR001082; Pilin.
 DR Pfam: PF00114; pilin; 1.
 DR ProDom: PD000666; Pilin; 1.
 SQ SEQUENCE 136 AA; 14302 MW; A834A9C4EA7C63B1 CRC64;

Query Match 17.5%; Score 107; DB 2; Length 136;
 Best Local Similarity 31.2%; Pred. No. 0.036;
 Matches 35; Conservative 15; Mismatches 48; Indels 14; Gaps 4;

OY 8 ARSEGASALATINPLKTYEESLSRGISGKIKIGTASTATFAYAGVDPANKLGVIAV 67
 DB 35 ASQVYAGLAETINPKGTQYEVALLNEG-----KTVADITF-LGLKSPSERC-TIAP 83

OY 68 AIEDSGADITFTFQGTSSPKNATKVTILNRTADGVWACKSTQDPMFTPKG 119
 DB 84 ITALSATGTIECTLKGN---GVVGKKVTLTRANSGTWCKTDAKKVAPAG 132

RESULT 10
 OYAP36 PRELIMINARY; PRT; 131 AA.

AC OYAP36;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE FIMBRIAL SUBUNIT (FRAGMENT).
 GN FIMA.
 OS *Bacteroides nodosus* (Dichelobacter nodosus).
 OC Bacteria; Proteobacteria; gamma subdivision; Cardiobacteriaceae;
 OC Dichelobacter.
 OX NCBI_TaxID=870;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhou H., Hickford J.G.H.;
 RT "Dichelobacter nodosus fimbrial subunit gene";
 RL Submitted (OCT-2000) to the EMBL/GenBank/DDbJ databases.
 DR EMBL: AF31610; AAK00323.1; -
 FT NON_TER
 SQ SEQUENCE 131 AA; 13933 MW; 54D6D20DCB1ABD CRC64;

Query Match 17.2%; Score 105.5; DB 2; Length 131;
 Best Local Similarity 27.6%; Pred. No. 0.046;
 Matches 34; Conservative 19; Mismatches 53; Indels 17; Gaps 4;

OY 8 ARSEGASALATINPLKTYEESLSRGISGKIKIGTASTAT--ETVAGVDPANKLGVIA 65
 DB 10 ARSQVSRVMSSETGMRTAETCVLDGKADKCTIGMTGSLDLGFTAGTGSTAAATGCT 69

OY 66 AVAIEDSGA---GDTFTFQGTSSPKNAT-----KVITLNRADGVWACKSTQDPMFT 116
 DB 70 GITIKYPAADDEGNIVATF-----GRNAAAIKPOLTWRSKSGTWCATVBAKFO 123

OY 117 PKG 119
 DB 124 PTC 126

RESULT 11
 OYAP36 PRELIMINARY; PRT; 157 AA.
 AC OYAP36;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE PILIN.

OS Dichelobacter nodosus H1.
 OC Bacteria; Proteobacteria; gamma subdivision; Cardiobacteriaceae;
 OC Dichelobacter.
 OX NCBI_TaxID=46911;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BN265;
 RA MEDLINE=90155189; PubMed=2621448;
 RA Hoyle P.A., Ellemann T.C., McKern N.M., Stewart D.J.;
 RT "Sequence of pilin from *Bacteroides nodosus* 351 (Serogroup H) and
 RT implications for serogroup classification.";
 RL J. Gen. Microbiol. 135:113-1122(1989).
 CC -I- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
 CC NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
 CC CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
 CC CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS (BY
 CC SIMILARITY).
 CC -I- SIMILARITY: BELONGS TO THE FIMBRIAL PROTEIN (N-ME-PHE)PILIN
 CC FAMILY.
 DR EMBL: M26979; AAA98742.1; -
 DR HSSP: O53391; 1KB8.
 DR InterPro: IPR001082; Pilin.
 DR InterPro: IPR001120; Prok_N_methyltn.
 DR Pfam: PF00114; pilin; 1.
 DR ProDom: PD000666; Pilin; 1.
 DR PROSITE: PS00409; PROKAR_NTER_METHYL; 1.
 KW Fimbria; Methylation.
 FT MOD_RES
 SQ SEQUENCE 157 AA; 16702 MW; 63E01952511E0967 CRC64;

Query Match 17.2%; Score 105.5; DB 2; Length 157;
 Best Local Similarity 27.6%; Pred. No. 0.057;
 Matches 34; Conservative 19; Mismatches 53; Indels 17; Gaps 4;

OY 8 ARSEGASALATINPLKTYEESLSRGISGKIKIGTASTAT--ETVAGVDPANKLGVIA 65
 DB 36 ARSQVSRVMSSETGMRTAETCVLDGKADKCTIGMTGSLDLGFTAGTGSTAAATGCT 95

OY 66 AVAIEDSGA---GDTFTFQGTSSPKNAT-----KVITLNRADGVWACKSTQDPMFT 116
 DB 96 GITIKYPAADDEGNIVATF-----GRNAAAIKPOLTWRSKSGTWCATVBAKFO 149

OY 117 PKG 119
 DB 150 PTC 152

RESULT 12
 OYAP36 PRELIMINARY; PRT; 159 AA.
 AC OYAP36;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE PREPILIN.
 OS *Moraxella bovis*.
 OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae; Moraxella.
 OX NCBI_TaxID=476;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-TAT849 / SEROGROUP E;
 RA MEDLINE=94327452; PubMed=8051000;
 RA Atwell J.L., Tennent J.M., Lepper A.W., Ellemann T.C.;
 RT "Characterization of pilin genes from seven serologically defined
 RT prototype strains of *Moraxella bovis*.";
 RL J. Bacteriol. 176:4875-4882(1994).
 CC -I- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
 CC NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
 CC CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
 CC CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS (BY
 CC SIMILARITY).
 CC -I- SIMILARITY: BELONGS TO THE FIMBRIAL PROTEIN (N-ME-PHE)PILIN

CC FAMILY.
 DR EMBL: I32972; AAA53561.1;
 DR InterPro: IPR001082; PiliN.
 DR InterPro: IPR001120; Prok_N_methyln.
 DR Pfam: PF00114; PiliN; 1.
 DR ProDom: PD000666; PiliN; 1.
 DR ProSITE: PS00409; PROKAR_NTER_METHYL; 1.
 DR Fimbrin; Methylation.
 FT MOD_RES 7;
 SEQUENCE 159 AA; 16534 MW; F40828A90E993089 CRC64;

Query Match 16.7%; Score 102.5; DB 2; Length 159;
 Best Local Similarity 27.6%; Pred. No. 0.11;
 Matches 35; Conservative 21; Mismatches 50; Indels 21; Gaps 5;

QY 8 ARSEASALATINPLKTVESLSRG-----TAGSKIKIGTTASTATETVAGVERDA 59
 DB 35 SKSOTTRVVGELAAKTVADALAEKGPVLEASSTKENIGLITSENSAT-----PRS 89
 QY 60 NKLGIYAV-AIEDSGAGDITFTFGTSSPKNATKVTILNRTADGCVACK-----STOD 112
 DB 90 NLMESVSLGFDSDSGSGISATL-GGNANKDIATVTSQNTDGVWTCVDGKAPRYK 148
 QY 113 PMFTPKG 119
 DB 149 AKFTPAG 155

RESULT 13
 Q9APK5 PRELIMINARY; PRT; 145 AA.
 AC Q9APK5;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE FIMA PRECURSOR.
 OS Xanthomonas hyacinthi.
 OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
 OC Xanthomonas.
 OX NCBI_TaxID=56455;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=1115722;
 RA van Doorn J.J., Hollinger T.C., Oudega B.;
 RT "Analysis of the Type IV Fimbrial-Subunit Gene fima of Xanthomonas
 RT hyacinthi: Application in PCR-Mediated Detection of Yellow Disease in
 RT hyacinths."
 RL Appl. Environ. Microbiol. 67:598-607(2001).
 DR EMBL: AF281159; AK11163.1;
 DR SEQUENCE 145 AA; 14911 MW; BB521BA0B59D68E1 CRC64;

Query Match 16.7%; Score 102; DB 2; Length 145;
 Best Local Similarity 30.2%; Pred. No. 0.1;
 Matches 32; Conservative 17; Mismatches 37; Indels 20; Gaps 5;

QY 8 ARSEASALATINPLKTVESLSRGISAGSKIKIGTTASTATETVAGVERDANKLGIVAV 67
 DB 35 ARSOVSAGLAETTPGKVAQETRIAEQ-----KATTTQADVGAGASISRG-IAV 83
 QY 68 AIEDSGAGDITFTFGTSSPKNATKVTILNRTAD-----GVMAC 107
 DB 84 SYDPSGAATITCTLK-GNAQINGQT--IQWTRADTANGTGVWTC 126

RESULT 14
 Q9PAH9 PRELIMINARY; PRT; 148 AA.
 AC Q9PAH9;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

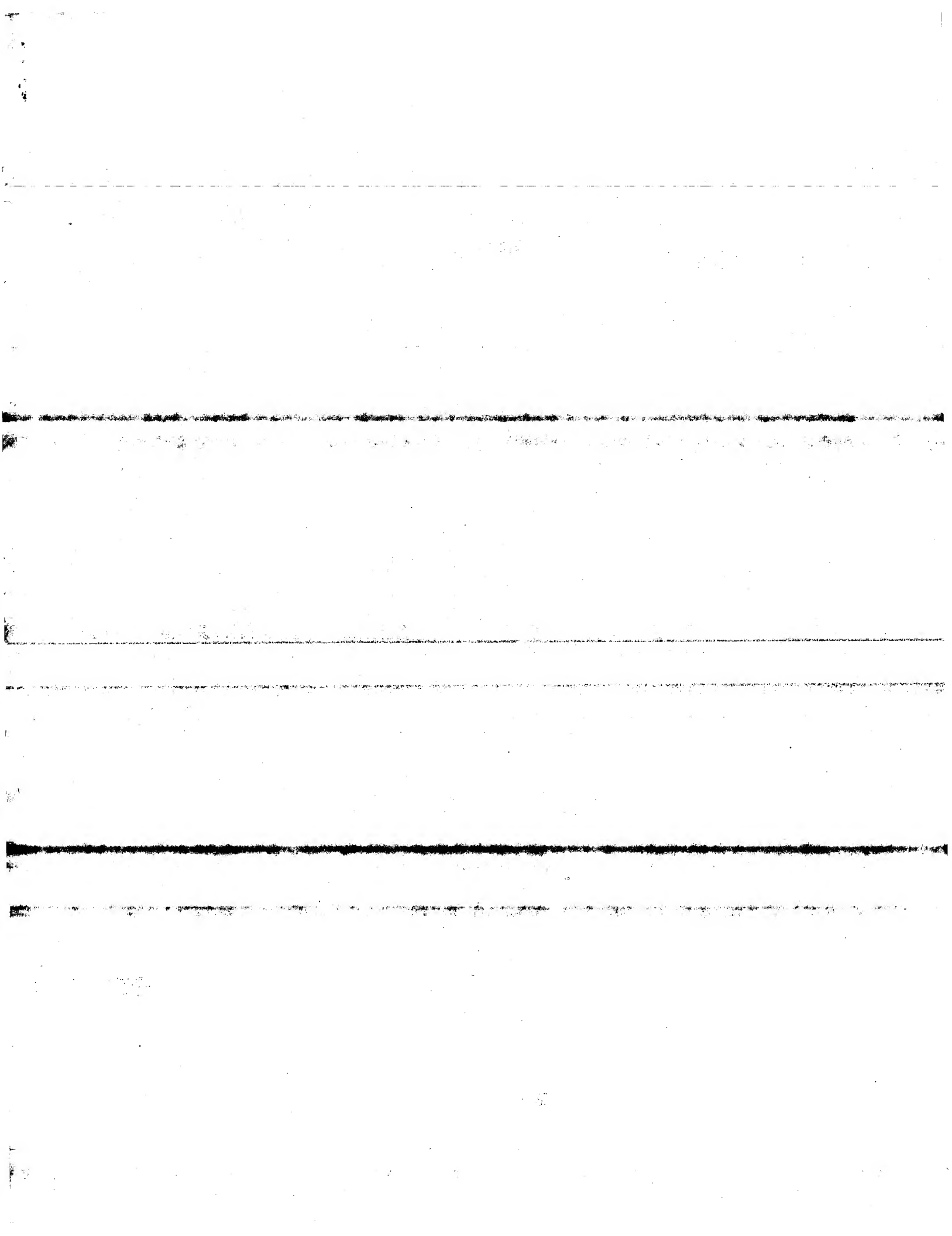
DE FIMBRIAL PROTEIN.
 GN XF2539.
 OS Xylella fastidiosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
 OC Xylella.
 OX NCBI_TaxID=2371;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=9A5C;
 RX MEDLINE=20365717; PubMed=10910347;
 RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
 RA Alvaranga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
 RA Barreto M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Bionnes M.R.S.,
 RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carer H.,
 RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa Neto C.M.,
 RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
 RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
 RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
 RA Gardner M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
 RA Ho P.L., Hohnsels J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
 RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
 RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
 RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
 RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
 RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
 RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
 RA Nhani A., Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
 RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
 RA Peixoto B.R., Pereira P.G., Rodrigues V., de Rosa A.J.M.,
 RA Quaggio R.B., Roberto P.G., Santelli R.V., Sawasaki H.E.,
 RA de Rosa V.E., Jr., de Sa R.G., Santelli R.V., Silva W.A., Jr.,
 RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A., Jr.,
 RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
 RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tshako M.H.,
 RA Vallada H., Van Sluys M.A., Verjovsky-Almeida S., Vettore A.L.,
 RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
 RT "The genome sequence of the plant pathogen Xylella fastidiosa."
 RL Nature 406:151-159(2000).
 DR EMBL: AE004061; AAF85336.1;
 DR InterPro: IPR002416; Bac_GSPH.
 DR InterPro: IPR001082; PiliN.
 DR Pfam: PF00114; PiliN; 1.
 DR PRINTS: PR00885; BACTERIALGSPH.
 DR ProDom: PD000666; PiliN; 1.
 KM Complete proteome.
 SO SEQUENCE 148 AA; 13363 MW; A70148CEDC4DC30E CRC64;

Query Match 16.7%; Score 102; DB 2; Length 148;
 Best Local Similarity 29.8%; Pred. No. 0.11;
 Matches 34; Conservative 16; Mismatches 38; Indels 26; Gaps 5;

QY 8 ARSEASALATINPLKTVESLSRGISAGSKIKIGTTASTATETVAGVERDANKLGIVAV 67
 DB 35 ARSOLTAALADITPGKVAQESLIADG-----KSTSNASDILRTDITTCG-ITV 82
 QY 68 AIEDSGAGDITFTFGTSSPKNATKVTILNRTAD-----GVMACKST 110
 DB 83 KVDADGANTITCKVK-GNSQVND--KITAMDRTSDNAGTNGVNGGVWTCSS 133

RESULT 15
 Q59794 PRELIMINARY; PRT; 154 AA.
 AC Q59794;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE FIMBRIAL PROTEIN PRECURSOR (PILIN) (STRAIN 577B).
 GN PILA OR FIMA.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.

XX	NCBI_TaxID=287;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=577B;			
RX	MEDLINE=94131566; PubMed=7507890;			
RA	Castric P.A., Deal C.D.;			
RT	"Differentiation of <i>Pseudomonas aeruginosa</i> pili based on sequence and B-cell epitope analyses."			
RL	Infect. Immun. 62:371-376(1994).			
CC	-1- SUBUNIT THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4 NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH. THEY			
CC	CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.			
CC	-1- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.			
DR	EMBL; S68101; AAC60461.1; -			
DR	HSSP; P02974; 2PIL.			
DR	InterPro: IPR001082; PiliH.			
DR	InterPro: IPR001120; Prok_N_methylCh.			
DR	Pfam; PF00114; PiliH; 1.			
DR	ProDom; PD000666; PiliH; 1.			
DR	PROSITE; PS00409; PROKAR_NTER_METHYL; 1.			
FM	Fimbria; Methylation.			
FT	PROPEP	1		
FT	CHAIN	7	154	FIMBRIAL PROTEIN.
FT	DISULFID	133	151	BY SIMILARITY.
FT	MOD_RES	7		METHYLATION (BY SIMILARITY).
SQ	SEQUENCE	154 AA;	16317 MW;	52A0A56725135719 CRC64;



GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 8, 2002, 15:25:10 ; Search time 32.48 Seconds
(without alignments)
84.526 Million cell updates/sec

Title: US-09-865-159-6

Perfect score: 612
Sequence: 1 ALEGTFFARSEGASALATLN.....GWACKSTODPMFTPKGSDN 122

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008

Listing first 45 summaries

Database :

Issued_Patents_AA.*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PTCUS.COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	102.5	16.7	154	3	US-08-486-099-108 Sequence 108, App
2	102.5	16.7	154	3	US-08-360-107A-118 Sequence 118, App
3	102.5	16.7	154	3	US-08-484-223B-108 Sequence 108, App
4	102.5	16.7	154	3	US-08-919-597-108 Sequence 108, App
5	102.5	16.7	154	3	US-08-475-668A-108 Sequence 108, App
6	102.5	16.7	154	3	US-08-485-551A-108 Sequence 108, App
7	102.5	16.7	154	3	US-08-471-913A-108 Sequence 108, App
8	102.5	16.7	154	4	US-08-485-264A-108 Sequence 108, App
9	90	14.7	17	1	US-08-084-739-6 Sequence 6, Appli
10	90	14.7	17	1	US-07-638-492-3 Sequence 3, Appli
11	76	12.4	413	1	US-08-295-676A-2 Sequence 2, Appli
12	76	12.4	413	1	US-08-750-077-6 Sequence 6, Appli
13	76	12.4	413	2	US-08-948-591-2 Sequence 2, Appli
14	75	12.3	14	6	5445818-3 Patent No. 5445818
15	74.5	12.0	639	2	US-08-637-899-1 Sequence 1, Appli
16	73.5	12.0	1026	2	US-08-542-003-6 Sequence 6, Appli
17	73.5	12.0	1026	2	US-08-322-760A-6 Sequence 6, Appli
18	71.5	11.7	268	2	US-09-135-658-1 Sequence 1, Appli
19	70.5	11.5	264	2	US-08-494-907-6 Sequence 6, Appli
20	70.5	11.5	264	5	PCT-US96-10986-6 Sequence 6, Appli
21	70	11.4	659	4	US-08-894-818B-5 Sequence 5, Appli
22	69.5	11.4	272	2	US-08-441-857-4 Sequence 4, Appli
23	69.5	11.4	272	2	US-08-193-159-4 Sequence 4, Appli
24	69.5	11.4	337	2	US-08-441-857-8 Sequence 8, Appli
25	69.5	11.4	337	3	US-08-193-159-8 Sequence 8, Appli
26	69.5	11.4	378	1	US-07-772-087-3 Sequence 3, Appli
27	68.5	11.2	1477	1	US-08-038-682-4 Sequence 4, Appli

28	68.5	11.2	1477	1	US-08-302-832-4 Sequence 4, Appli
29	68.5	11.2	1477	2	US-08-530-198-4 Sequence 4, Appli
30	68.5	11.2	1477	2	US-08-469-880-4 Sequence 4, Appli
31	68.5	11.2	1477	2	US-08-728-470-4 Sequence 4, Appli
32	68.5	11.2	1477	2	US-08-617-697-4 Sequence 4, Appli
33	68.5	11.2	1477	4	US-08-719-641-4 Sequence 4, Appli
34	68	11.1	607	1	US-08-409-995-6 Sequence 6, Appli
35	68	11.1	607	3	US-08-685-467-6 Sequence 6, Appli
36	68	11.1	607	4	US-08-913-942-6 Sequence 6, Appli
37	68	11.1	1584	4	US-09-251-645-6 Sequence 6, Appli
38	68	11.1	1912	1	US-08-409-995-4 Sequence 4, Appli
39	68	11.1	1912	3	US-08-685-467-4 Sequence 4, Appli
40	68	11.1	2353	4	US-09-377-155-33 Sequence 33, Appli
41	68	11.1	2353	4	US-08-913-942-4 Sequence 4, Appli
42	67	10.9	761	1	US-07-906-395-2 Sequence 2, Appli
43	67	10.9	761	1	US-08-192-632-2 Sequence 2, Appli
44	67	10.9	761	1	US-08-710-676-2 Sequence 2, Appli
45	67	10.9	761	3	US-09-099-902B-2 Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-486-099-108
Sequence 108, Application US/08486099
Patent No. 6013263
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION ASSOCIATED EVENTS, INCLUDING HEPATITIS
B VIRUS TRANSMISSION
TITLE OF INVENTION: B VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,099
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-031
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 154 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-486-099-108

Query Match 16.7%; Score 102.5; DB 3; Length 154;
 Best Local Similarity 30.2%; Pred. No. 6.1e-05;
 Matches 35; Conservative 18; Mismatches 42; Indels 21; Gaps 5;

QY 8 ARSGASALATINPLKTTVESLSRG--IAGS-----KIKIGTTASTATETAGVEPDA 59
 DB 35 ARQVTRAVSEVSAIKTAESAILLEGKEIVSATPKDQYDIGFTSTLTD----- 85

QY 60 NKLGIVAVAIEDSGAGDITFTFGTSSPKNATK--VITLNRADGVWACKSTODP 113
 DB 86 -GSGKSOIQVTDNODGTVELVATLGKSS-GSAIKGAVITVSRKNDGVWCKITKTP 139

RESULT 2

US-08-360-107A-118
 ; Sequence 118, Application US/08360107A
 ; Patent No. 6017536

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.
 APPLICANT: Matthews, Thomas J.
 APPLICANT: Wild, Carl T.
 APPLICANT: Barney, Shawn O.
 APPLICANT: Lambert, Dennis M.
 APPLICANT: Langlois, Stephen R.
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
 TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
 NUMBER OF SEQUENCES: 149
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/360.107A
 FILING DATE: 20-DEC-1994
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: 7872-013
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-9741/8864
 TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 118:

SEQUENCE CHARACTERISTICS:
 LENGTH: 154 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 US-08-360-107A-118

Query Match 16.7%; Score 102.5; DB 3; Length 154;
 Best Local Similarity 30.2%; Pred. No. 6.1e-05;
 Matches 35; Conservative 18; Mismatches 42; Indels 21; Gaps 5;

QY 8 ARSGASALATINPLKTTVESLSRG--IAGS-----KIKIGTTASTATETAGVEPDA 59
 DB 35 ARQVTRAVSEVSAIKTAESAILLEGKEIVSATPKDQYDIGFTSTLTD----- 85

QY 60 NKLGIVAVAIEDSGAGDITFTFGTSSPKNATK--VITLNRADGVWACKSTODP 113
 DB 86 -GSGKSOIQVTDNODGTVELVATLGKSS-GSAIKGAVITVSRKNDGVWCKITKTP 139

DB 86 -GSGKSOIQVTDNODGTVELVATLGKSS-GSAIKGAVITVSRKNDGVWCKITKTP 139

RESULT 3

US-08-484-223B-108
 ; Sequence 108, Application US/08484223B
 ; Patent No. 6020459

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.
 APPLICANT: Matthews, Thomas J.
 APPLICANT: Wild, Carl T.
 APPLICANT: Barney, Shawn O.
 APPLICANT: Lambert, Dennis M.
 APPLICANT: Peteway, Stephen R.
 APPLICANT: Langlois, Alphonse J.
 TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
 TITLE OF INVENTION: TRANSMISSION
 NUMBER OF SEQUENCES: 245
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds LLP
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/484.223B
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: 7872-029
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-9741/8864
 TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 108:

SEQUENCE CHARACTERISTICS:
 LENGTH: 154 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 US-08-484-223B-108

Query Match 16.7%; Score 102.5; DB 3; Length 154;
 Best Local Similarity 30.2%; Pred. No. 6.1e-05;
 Matches 35; Conservative 18; Mismatches 42; Indels 21; Gaps 5;

QY 8 ARSGASALATINPLKTTVESLSRG--IAGS-----KIKIGTTASTATETAGVEPDA 59
 DB 35 ARQVTRAVSEVSAIKTAESAILLEGKEIVSATPKDQYDIGFTSTLTD----- 85

QY 60 NKLGIVAVAIEDSGAGDITFTFGTSSPKNATK--VITLNRADGVWACKSTODP 113
 DB 86 -GSGKSOIQVTDNODGTVELVATLGKSS-GSAIKGAVITVSRKNDGVWCKITKTP 139

RESULT 4

US-08-919-597-108
 ; Sequence 108, Application US/08919597
 ; Patent No. 6054265

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.
 APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.
 APPLICANT: Barney, Shawn O.
 APPLICANT: Lambert, Dennis M.
 APPLICANT: Letteway, Stephen R.
 APPLICANT: Langlois, Alphonse J.
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
 TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
 TITLE OF INVENTION: TRANSMISSION
 NUMBER OF SEQUENCES: 273
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10036-2711
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentln Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/919,597
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/470,896
 FILING DATE: 06-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Coruzzi, Laura A.
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: 7872-020
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-9741/8684
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 108:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 154 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 US-08-919-597-108

```

STREET 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,668A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 154 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-475-668A-108

```

```

Query Match      16.7%: Score 102.5; DB 3; Length 154;
Best Local Similarity 30.2%; Pred. No.6.1e-05;
Matches 35; Conservative 18; Mismatches 42; Indels 21; Gaps 5

QY      8 ARSEGASALATINPLKTFVEESLSRG--IAGS-----KIKIGTASTPTETFYAGVPEPA 59
       |||: |: |: |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: |
Db      35 ARTQTTRAVSESAKTTAEASALIEGKEIVSSATPKDQYDIGFTSLTD----- 85

QY      60 NKLGVIAVAIEDSGAGDITFTFGTSSPKNATK--VTILNTADGWACKSTODP 113
       | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      86 -GSCKSQIQIVDMDGVELVATLKSS-GSAIKAVLTVSRKNKGWMMCKITKTP 139

RESULT      5
US-08-475-668A-108
; Sequence 108, Application US/08475668A
; Patent No. 6060065
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Peteway, Stephen R.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP

```

[illegible]

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485, 551A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-023
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 154 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-485-551A-108

Query Match 16.7%; Score 102.5; DB 3; Length 154;
Best Local Similarity 30.2%; Pred. No. 6.1e-05;
Matches 35; Conservative 18; Mismatches 42; Indels 21; Gaps 5;

OY 8 ARSEGASALATINPLKTYVESLSRG--TAGS-----KIKIGTASTATETVAGVEPDA 59
DB 35 ARTQVTRAVSEVSAALTAESAILEGKEIVSATPRKQYDIDIGFTSTLID----- 85
OY 60 NKLGVAIVAEISGAGDITFTGTSSPRKMAT--VITLNRADGVWACKSTQDP 113
DB 86 -GSGKSOIQVTDNQDSTVELVATLGKSS-GSAIKGAVITVSRKNDGVWCKITKTP 139

RESULT 7
US-08-471-913A-108
Sequence 108, Application US/08471913A
Patent No. 6093794
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
NUMBER OF SEQUENCES: 214
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,913A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 154 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-471-913A-108

Query Match 16.7%; Score 102.5; DB 3; Length 154;
Best Local Similarity 30.2%; Pred. No. 6.1e-05;
Matches 35; Conservative 18; Mismatches 42; Indels 21; Gaps 5;

OY 8 ARSEGASALATINPLKTYVESLSRG--TAGS-----KIKIGTASTATETVAGVEPDA 59
DB 35 ARTQVTRAVSEVSAALTAESAILEGKEIVSATPRKQYDIDIGFTSTLID----- 85
OY 60 NKLGVAIVAEISGAGDITFTGTSSPRKMAT--VITLNRADGVWACKSTQDP 113
DB 86 -GSGKSOIQVTDNQDSTVELVATLGKSS-GSAIKGAVITVSRKNDGVWCKITKTP 139

RESULT 8
US-08-485-264A-108
Sequence 108, Application US/08485264A
Patent No. 6228983
GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING
NUMBER OF SEQUENCES: 232
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,264A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-021
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 154 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-485-264A-108

Query Match 16.7%; Score 102.5; DB 4; Length 154;
Best Local Similarity 30.2%; Pred. No. 6.1e-05;
Matches 35; Conservative 16; Mismatches 42; Indels 21; Gaps 5;

OY 8 ARSGASALATINPLKTTVESLSRG--TACS-----KIKIGTATATETVAGVEPDA 59
Db 35 ARTQVTRAVSEVSAIKTAESAIEGKEIVSSATPKDQYDIGFESTILD----- 85
OY 60 NKLGVIAVIEDSGAGDITTFQGTSSPKNATK--VITLNRFDGVMACKSTODP 113
Db 86 -GSGKSOIQVTDNODGVEIVATLGKSS-GSAIKGAVTVSRKNDGVNCKITKTP 139

RESULT 9

US-08-084-739-6
Sequence 6, Application US/08084739
Patent No. 5468484
GENERAL INFORMATION:
APPLICANT: Hodges, Robert S.
APPLICANT: Irvin, Randall T.
APPLICANT: Paranchych, William
APPLICANT: Sokol, Pamela A.
APPLICANT: Woods, Donald E.
TITLE OF INVENTION: Pseudomonas Exoenzyme S Peptide
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/084,739
FILING DATE: 28-JUN-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/721,759
FILING DATE: 25-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8900-0004.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: both
MOLECULE TYPE: Peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: PAO, Fig. 8
US-08-084-739-6

Query Match 14.7%; Score 90; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 8.2e-05;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 106 ACKSTODPMFTPKGSDN 122
Db 1 ACKSTODPMFTPKGCDN 17

RESULT 10
US-07-638-492-3
Sequence 3, Application US/07638492
Patent No. 5494672

GENERAL INFORMATION:
APPLICANT: Hodges, Robert S.
APPLICANT: Paranchych, William
APPLICANT: Irvin, Randall T.
APPLICANT: Lee, Kok K.
APPLICANT: Parimi, Sastiy A.
APPLICANT: Zoutman, Dick E.
APPLICANT: Wong, Mah Y.
TITLE OF INVENTION: Pseudomonas Peptide Composition and
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/638,492
FILING DATE: 04-JAN-1991
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8900-0002.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: peptide 3
US-07-638-492-3

Query Match 14.7%; Score 90; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 8.2e-05;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 106 ACKSTODPMFTPKGSDN 122
Db 1 ACKSTODPMFTPKGCDN 17

RESULT 11
US-08-295-676A-2
Sequence 2, Application US/08295676A
Patent No. 5677172
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: A method for production of proteins in
yeast
NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Birch, Stewart, Kolasch and Birch
 STREET: P.O. Box 747
 CITY: Falls Church
 STATE: VA
 COUNTRY: USA
 ZIP: 22040-0747
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/295,676A
 FILING DATE: 09-SEPT-1994
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 413 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-295-676A-2

Query Match 12.4%; Score 76; DB 1; Length 413;
 Best Local Similarity 27.4%; Pred. No. 0.45;
 Matches 37; Conservative 21; Mismatches 43; Indels 34; Gaps 8;

DB 5 TEFARSEGASALATINPLKTYVESLSRGISGSKIR-----IG-----TTASTATET 51
 40 TDYASTFGIA---VPISTTSASSAATTTASKAKRAASQIGDGVQAATTTASVSKS 95
 QY 52 YAGVEDANKLG-----VIAVAIEDSGAGDITFTPTGTSSPKNTKVTITNRAD 102
 DB 96 TAAA--VSQIDGQIQATTTKTTAAVSOIGDQIQAT--TKTTSK--TTAAVSQISD 148
 QY 103 G-VMAKSTQDPMFT 116
 DB 149 GQIQATTTTLAPKST 163

RESULT 12
 US-08-750-077-6
 Sequence 6, Application US/08750077
 Patent No. 5783423
 GENERAL INFORMATION:
 APPLICANT: Wood, Patricia C
 APPLICANT: Quirk, Alan V
 TITLE OF INVENTION: Yeast Strains
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Centeon LLC
 STREET: 1020 First Avenue
 CITY: King of Prussia
 COUNTRY: USA
 ZIP: PA 19406-1310
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/750,077
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9411356.0
 FILING DATE: 07-JUN-1994
 PRIOR APPLICATION NUMBER: PCT/GB95/01317
 FILING DATE: 07-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Moore, Steven J

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (610) 878 4073
 TELEFAX: (610) 878 4221
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 413 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-750-077-6

Query Match 12.4%; Score 76; DB 1; Length 413;
 Best Local Similarity 27.4%; Pred. No. 0.45;
 Matches 37; Conservative 21; Mismatches 43; Indels 34; Gaps 8;

DB 5 TEFARSEGASALATINPLKTYVESLSRGISGSKIR-----IG-----TTASTATET 51
 40 TDYASTFGIA---VPISTTSASSAATTTASKAKRAASQIGDGVQAATTTASVSKS 95
 QY 52 YAGVEDANKLG-----VIAVAIEDSGAGDITFTPTGTSSPKNTKVTITNRAD 102
 DB 96 TAAA--VSQIDGQIQATTTKTTAAVSOIGDQIQAT--TKTTSK--TTAAVSQISD 148
 QY 103 G-VMAKSTQDPMFT 116
 DB 149 GQIQATTTTLAPKST 163

RESULT 13
 US-08-948-591-2
 Sequence 2, Application US/08948591
 Patent No. 5939287
 GENERAL INFORMATION:
 APPLICANT:
 TITLE OF INVENTION: A method for production of proteins in
 NUMBER OF SEQUENCES: 21
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Birch, Stewart, Kolasch and Birch
 STREET: P.O. Box 747
 CITY: Falls Church
 STATE: VA
 COUNTRY: USA
 ZIP: 22040-0747
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/948,591
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/295,676
 FILING DATE: 09-SEPT-1994
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 413 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-948-591-2

Query Match 12.4%; Score 76; DB 2; Length 413;
 Best Local Similarity 27.4%; Pred. No. 0.45;
 Matches 37; Conservative 21; Mismatches 43; Indels 34; Gaps 8;

DB 5 TEFARSEGASALATINPLKTYVESLSRGISGSKIR-----IG-----TTASTATET 51
 40 TDYASTFGIA---VPISTTSASSAATTTASKAKRAASQIGDGVQAATTTASVSKS 95

Fri Feb 8 15:44:52 2002

us-09-865-159-6.ra1

Page 7

QY 52 YAGVDPANKLG-----VIAVAIEDSGAGDITFTFGTSSPKNAFKVITLNRPAD 102
Db 96 TAAA--VSQIDGQIQATTTKTTAAVSOIGDQIQAT--TKTSAK--TTAAVSOISD 148
QY 103 G-VMAKSTODPMFT 116
Db 149 GQIQATTTTLAPKST 163

RESULT 14
5445818-3
: Patent No. 5445818
: APPLICANT: HODGES, ROBERT S.; PARANCHYCH, WILLIAM; LEE, KOK K.;
: PARMET, SASTRY A.; IRVIN, RANDALL T.; DOIG, PETER C.
: TITLE OF INVENTION: SYNTHETIC PSEUDOMONAS AERUGINOSA PILIN
: PEPTIDE VACCINE AND METHOD OF USE
: NUMBER OF SEQUENCES: 10
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/927,797
: FILING DATE: 10-AUG-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 344,565
: FILING DATE: 28-APR-1989
: SEQ ID NO: 3:
: LENGTH: 14
5445818-3

Query Match 12.3%; Score 75; DB 6; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0042;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 CKSTODPMFTPKG 119
Db 1 CKSTODPMFTPKG 13

RESULT 15
US-08-637-899-1
: Sequence 1, Application US/08637899
: Patent No. 5908772
: GENERAL INFORMATION:
: APPLICANT: Mitla, Masanori
: APPLICANT: Sano, Mutsumi
: APPLICANT: Kato, Ikunoshin
: TITLE OF INVENTION: Gene Encoding Lacto-N-Biosidase
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Birch, Stewart, Kolasch and Birch
: STREET: P.O. Box 747
: CITY: Falls Church
: STATE: VA
: COUNTRY: USA
: ZIP: 22040-0747
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/637,899
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Weiner, Marc S
: REGISTRATION NUMBER: 32,181
: REFERENCE/DOCKET NUMBER: 1422-252P
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (703) 205-8000
: TELEFAX: (703) 205-8050
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:

LENGTH: 639 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-637-899-1

Query Match 12.2%; Score 74.5; DB 2; Length 639;
Best Local Similarity 25.2%; Pred. No. 1.3;
Matches 32; Conservative 14; Mismatches 38; Indels 43; Gaps 5;
QY 28 ESLSGIA--GSKIKI--GTTASTATE-----TTAGVVP 57
Db 432 QTLTGAAALTGAKISLWPDAAAEFTENEVEKVPMPLEFVAQATWCGPSPPTAGFEA 491
QY 58 DANKLG-----VIAVAIED-----SGAGDITFTFGTSSPKNAFKVITLNRPADGV 104
Db 492 LARKIGHAGMENTDRTPADGTYRLTTGAKALAPADAGVSLVNSAASMALTRADGV 551
QY 105 WACKSTQ 111
Db 552 YTVRSTE 558

Search completed: February 8, 2002, 15:25:11
Job time: 116 sec

Fri Feb 8 15:44:52 2002

us-09-865-159-6.rai

Page 8

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 8, 2002, 15:32:38 ; Search time 353.09 Seconds
(without alignments)
95,936 Million cell updates/sec

Title: US-09-865-159-6

Perfect score: 612

Sequence: 1 ALEGTFAFSEGSALATIN.....GVACKSTODPMFTPKGSDN 122

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3148936 seqs, 277657034 residues

Total number of hits satisfying chosen parameters: 3148936

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA Main:*

1: /cgn2_6/ptodata/2/paa/PCRNUS.COMB.pep.*
2: /cgn2_6/ptodata/2/paa/US06.COMB.pep.*
3: /cgn2_6/ptodata/2/paa/US07.COMB.pep.*
4: /cgn2_6/ptodata/2/paa/US08.COMB.pep.*
5: /cgn2_6/ptodata/2/paa/US09.COMB.pep.*
6: /cgn2_6/ptodata/2/paa/US091.COMB.pep.*
7: /cgn2_6/ptodata/2/paa/US092.COMB.pep.*
8: /cgn2_6/ptodata/2/paa/US093.COMB.pep.*
9: /cgn2_6/ptodata/2/paa/US094.COMB.pep.*
10: /cgn2_6/ptodata/2/paa/US095.COMB.pep.*
11: /cgn2_6/ptodata/2/paa/US096.COMB.pep.*
12: /cgn2_6/ptodata/2/paa/US097.COMB.pep.*
13: /cgn2_6/ptodata/2/paa/US098.COMB.pep.*
14: /cgn2_6/ptodata/2/paa/US099.COMB.pep.*
15: /cgn2_6/ptodata/2/paa/US0991.COMB.pep.*
16: /cgn2_6/ptodata/2/paa/US0992.COMB.pep.*
17: /cgn2_6/ptodata/2/paa/US0993.COMB.pep.*
18: /cgn2_6/ptodata/2/paa/US0994.COMB.pep.*
19: /cgn2_6/ptodata/2/paa/US0995.COMB.pep.*
20: /cgn2_6/ptodata/2/paa/US0996.COMB.pep.*
21: /cgn2_6/ptodata/2/paa/US0997.COMB.pep.*
22: /cgn2_6/ptodata/2/paa/US0998.COMB.pep.*
23: /cgn2_6/ptodata/2/paa/US0999.COMB.pep.*
24: /cgn2_6/ptodata/2/paa/US60.COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	612	100.0	122	17	US-09-329-884-6
2	593.5	97.0	168	17	US-09-329-884-22
3	592	96.7	168	17	US-09-329-884-20
4	325.5	53.2	123	17	US-09-329-884-4
5	307	50.2	169	17	US-09-329-884-14
6	305.5	49.9	169	17	US-09-329-884-12
7	137.5	22.1	139	22	US-09-848-616-140
8	135.5	22.1	139	22	US-09-848-616-140
9	133.5	21.8	127	17	US-09-329-884-10

	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45		
	114	112	109.5	109.5	102.5	102.5	102.5	102.5	102.5	102.5	102.5	102.5	102.5	102.5	102.5	102.5	102.5	102.5	102.5	102.5	99.5	91	90	90	90	89.5	84	83	83	83	83	83	83	82	82	82	82	
	18.6	18.3	17.9	17.9	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.3	14.9	14.7	14.7	14.7	14.6	13.7	13.6	13.6	13.6	13.6	13.6	13.6	13.4	13.4	13.4	13.4	
	53	3	169	17	129	17	154	8	154	8	154	8	154	8	154	8	154	8	154	13	19	3	17	17	17	17	17	17	20	24	24	24	24	24	24	24	24	24
	US-07-809-762A-27	US-09-328-352-6277	US-09-329-884-2	US-08-360-107-118	US-08-470-896-108	US-08-471-913-108	US-08-474-349-108	US-08-474-349A-108	US-08-475-668-108	US-08-484-223-108	US-08-484-223A-108	US-08-485-546-108	US-08-485-546A-108	US-08-487-266-108	US-08-487-266A-108	US-08-487-355-108	US-08-487-355A-108	US-08-919-600-108	US-07-809-762A-9	US-09-329-884-18	US-09-329-884-18	US-09-306-241-2	US-09-345-624-2	US-09-345-624A-2	US-09-328-884-16	PCT-US99-09034-34	US-09-619-049-1323	US-60-171-627-1917	US-60-173-464-25463	US-60-191-637-32827	US-60-191-681-35927	US-60-230-445-1072	US-60-175-8171-2197	US-60-167-217-22683	US-60-191-700-2136			
	Sequence 27, Appl	Sequence 6277, Ap	Sequence 2, Appl	Sequence 118, Appl	Sequence 108, Appl	Sequence 108, Appl	Sequence 108, Appl	Sequence 108, Appl	Sequence 108, Appl	Sequence 108, Appl	Sequence 108, Appl	Sequence 108, Appl	Sequence 108, Appl	Sequence 108, Appl	Sequence 108, Appl	Sequence 108, Appl	Sequence 108, Appl	Sequence 108, Appl	Sequence 9, Appl	Sequence 1917, Ap	Sequence 2, Appl	Sequence 2, Appl	Sequence 2, Appl	Sequence 16, Appl	Sequence 34, Appl	Sequence 1323, Ap	Sequence 1917, Ap	Sequence 25463, A	Sequence 32827, A	Sequence 25927, A	Sequence 1072, Ap	Sequence 2197, Ap	Sequence 22683, A	Sequence 2136, Ap				

ALIGNMENTS

RESULT 1

US-09-329-884-6

Sequence 6, Application US/09329884

GENERAL INFORMATION:

APPLICANT: Irvin, Randall T.

APPLICANT: Hodges, Robert S.

TITLE OF INVENTION: COMPOSITION AND METHOD

FILE REFERENCE: 8900-0008.30

CURRENT APPLICATION NUMBER: US/09/329, 884

CURRENT FILING DATE: 1999-06-11

EARLIER APPLICATION NUMBER: US 60/089, 155

NUMBER OF SEQ ID NOS: 22

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 6

LENGTH: 122

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-329-884-6

Query Match 100.0%; Score 612; DB 17; Length 122;

Best Local Similarity 100.0%; Pred. No. 8.4e-63;

Matches 122; Conservative 0; Mismatch 0; Indels 0; Gaps 0;

QY 1 ALEGTFAFSEGSALATINPLKTYVEESISRIASIKIKIGTATATETAGVPPDAN 60

DB 1 ALEGTFAFSEGSALATINPLKTYVEESISRIASIKIKIGTATATETAGVPPDAN 60

QY 61 KGVAVVAIEDSGAGDITTFQGTSSPKMATVITLNFADGVACKSTODPMFTPKGS 120

Db 61 KLGVAIAIEDSGAGDITFTFOTGTSSPKNATKVITLNRADGVWACKSTODPMFTPKGS 120
QY 121 DN 122
Db 121 DN 122

RESULT 2

US-09-329-884-22
Sequence 22, Application US/09329884
GENERAL INFORMATION:
APPLICANT: Irvin, Randall T.
APPLICANT: Hodges, Robert S.
TITLE OF INVENTION: PSEUDOMONAS TREATMENT
FILE REFERENCE: 8900-0008.30
CURRENT APPLICATION NUMBER: US/09/329,884
CURRENT FILING DATE: 1999-06-11
EARLIER APPLICATION NUMBER: US 60/089,155
EARLIER FILING DATE: 1998-06-12
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 22
LENGTH: 168
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-329-884-22

Query Match 97.0%; Score 593.5; DB 17; Length 168;
Best Local Similarity 96.8%; Pred. No. 1.9e-60;

Matches 121; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

QY 1 ALE---GTEPARSEGASALATINPLKTTVEESLSRGISGKIKIGTASTATETTYAGVBP 57
Db 44 ALKGGGGEARSEGASALATINPLKTTVEESLSRGISGKIKIGTASTATETTYAGVBP 103
QY 58 DANKLGVIAVAIEDSGAGDITFTFOTGTSSPKNATKVITLNRADGVWACKSTODPMFT 117
Db 104 DANKLGVIAVAIEDSGAGDITFTFOTGTSSPKNATKVITLNRADGVWACKSTODPMFT 163
QY 118 KGSND 122
Db 164 KGSND 168

RESULT 3

US-09-329-884-20
Sequence 20, Application US/09329884
GENERAL INFORMATION:
APPLICANT: Irvin, Randall T.
APPLICANT: Hodges, Robert S.
TITLE OF INVENTION: PSEUDOMONAS TREATMENT
FILE REFERENCE: 8900-0008.30
CURRENT APPLICATION NUMBER: US/09/329,884
CURRENT FILING DATE: 1999-06-11
EARLIER APPLICATION NUMBER: US 60/089,155
EARLIER FILING DATE: 1998-06-12
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 20
LENGTH: 168
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-329-884-20

Query Match 96.7%; Score 592; DB 17; Length 168;
Best Local Similarity 99.2%; Pred. No. 2.8e-60;

Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4 GTEPARSEGASALATINPLKTTVEESLSRGISGKIKIGTASTATETTYAGVBPDANKLG 63

Db 50 GGEARSEGASALATINPLKTTVEESLSRGISGKIKIGTASTATETTYAGVBPDANKLG 109
QY 64 VIAVAIEDSGAGDITFTFOTGTSSPKNATKVITLNRADGVWACKSTODPMFTPKGSND 122
Db 110 VIAVAIEDSGAGDITFTFOTGTSSPKNATKVITLNRADGVWACKSTODPMFTPKGSND 168

RESULT 4

US-09-329-884-4
Sequence 4, Application US/09329884
GENERAL INFORMATION:
APPLICANT: Irvin, Randall T.
APPLICANT: Hodges, Robert S.
TITLE OF INVENTION: PSEUDOMONAS TREATMENT
FILE REFERENCE: 8900-0008.30
CURRENT APPLICATION NUMBER: US/09/329,884
CURRENT FILING DATE: 1999-06-11
EARLIER APPLICATION NUMBER: US 60/089,155
EARLIER FILING DATE: 1998-06-12
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 123
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-329-884-4

Query Match 53.2%; Score 325.5; DB 17; Length 123;
Best Local Similarity 60.2%; Pred. No. 2e-29;

Matches 74; Conservative 11; Mismatches 31; Indels 7; Gaps 4;

QY 1 ALEGEFARSEGASALATINPLKTTVEESLSRGISGKIKIGTASTAT--ETTAGVBP 58
Db 1 ALEGEFARSEGASALATINPLKTTVEESLSRGISGKIKIGTASTATETTYAGVBP 57
QY 59 ANKLGVIAVAIEDS--GAGDITFTFOTGTSSPKNATKVITLNR--ADGVWACKSTODPMFT 116
Db 58 ANKLGVIAVAIEDS--GAGDITFTFOTGTSSPKNATKVITLNR--ADGVWACKSTODPMFT 117
QY 117 PKG 119
Db 118 PKG 120

RESULT 5

US-09-329-884-14
Sequence 14, Application US/09329884
GENERAL INFORMATION:
APPLICANT: Irvin, Randall T.
APPLICANT: Hodges, Robert S.
TITLE OF INVENTION: PSEUDOMONAS TREATMENT
FILE REFERENCE: 8900-0008.30
CURRENT APPLICATION NUMBER: US/09/329,884
CURRENT FILING DATE: 1999-06-11
EARLIER APPLICATION NUMBER: US 60/089,155
EARLIER FILING DATE: 1998-06-12
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 14
LENGTH: 169
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-329-884-14

Query Match 50.2%; Score 307; DB 17; Length 169;
Best Local Similarity 57.9%; Pred. No. 4.4e-27;

Matches 73; Conservative 11; Mismatches 32; Indels 10; Gaps 5;

```

OY      1 ALE---GEEFARSGASALATINPLKTTVEESLSRGTAGSKIKIGTAAST--ETVAGV 55
       | | | | | | | | | | :| | | | | | | | | | :| | | | |
Db     44 ALEGGGEFFARSBGASHASVNPLKTTFEALSRCMS---VASGTIEDATKEVP LGV 1000
                                     | ||||
OY      56 EPDANKLGVAVAIEDS-GACDITFEFTQGTSSPKNATKIYTILNT-ADGWMACKSTODP 113
       | | | | | | | | | | :| -| | | | :| | | | | | | | | | | | | |
Db     101 AAADNKLTCTIALKPDPADPTADITLFTEFMWGAGCPKNKGKITTLTRTAADGLMKCTSPDE 1608
                                      | |||
OY      114 MFPFGC 119
       | | | |
Db     161 QFIPIKC 166


RESULT        6
US-09-329-884-12
: Sequence 12, Application US-/09329884
GENERAL INFORMATION:
APPLICANT: Irvin, Randall T.
APPlicant: Hodges, Robert S.
TITLE OF INVENTION: PSEUDOMONAS TREATMENT
TITLE OF INVENTION: COMPOSITION AND METHOD
FILE REFERENCE: 8900-0008.30
CURRENT APPLICATION NUMBER: US-/09-/329, 884
CURRENT FILING DATE: 1999-06-11
EARLIER APPLICATION NUMBER: US 60/089,155
EARLIER FILING DATE: 1998-06-12
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 12
LENGTH: 169
TYPE: PRt
ORGANISM: Pseudomonas aeruginosa
US-09-329-884-12
```

	Query Match	Similarity	Score	DB	Length
Best Local	58.3%	Pred. No. 6	6e-27		
Matches	70	Conservative	11	Mismatches	32; Indels 7; Gaps 4
Qy	4	GGEFARSGASGLATINPLKTVVEESLSGIGASKRIKIGTASTAT--ETVAGVDEPDANK	61		
Db	50	GGEFARSGASGLATINPLKTVVEESLSGIGS--VKSTGTGEDATKKKEVPLGVADANK	106		
Qy	62	LGIVAVLEEDS--GADDITTFOTGATSSPNARKVILNLT--ADGVACKSTODPMETPKG	119		
Db	107	LGTVLAKPEDPADGTADITLTFMGGAGPNPKKRIITLTTPAADGLKCKTSDDOEPITPKG	166		

```

1 RESULT 7
2 US-09-329-884-8
3
4 Sequence 8, Application US/09329884
5
6 GENERAL INFORMATION:
7
8 APPLICANT: ILYIN, Randall T.
9
10 APPLICANT: Hodges, Robert S.
11
12 TITLE OF INVENTION: PSEUDOMONAS TREATMENT
13
14 TITLE OF INVENTION: COMPOSITION AND METHOD
15
16 FILE REFERENCE: 8900-0008, 30
17
18 CURRENT APPLICATION NUMBER: US/09/329,884
19
20 CURRENT FILING DATE: 1999-06-11
21
22 EARLIER APPLICATION NUMBER: US 60/089,155
23
24 EARLIER FILING DATE: 1998-06-12
25
26 NUMBER OF SEQ ID NOS: 22
27
28 SOFTWARE: PstSDQ for Windows Version 3.0
29
30 SEQ ID NO 8
31
32 LENGTH: 127
33
34 TYPE: PRT
35
36 ORGANISM: Pseudomonas aeruginosa
37
38 US-09-329-884-8

```

Query Match	22.58;	Score 137.5;	DB 17;	Length 127;
Best Local Similarity	34.18;	Pred. No. 1.6e-07;		
Matches	42;	Conservative 18;	Mismatches 42;	Indels 21;
				Gaps 5

[illegible]

```

RESULT 8
US-09-848-616-140
: Sequence 140, Application US/09848616
: GENERAL INFORMATION:
: APPLICANT: Sebbel, Peter
: APPLICANT: Dunant, Nicolas
: APPLICANT: Bachmann, Martin
: APPLICANT: Tissot, Alain
: APPLICANT: Lechner, Franziska
: TITLE OF INVENTION: Molecular Antigen Array
: FILE REFERENCE: 1700.0180002
: CURRENT APPLICATION NUMBER: US/09/848,616
: CURRENT FILING DATE: 2001-05-05
: NUMBER OF SEQ ID NOS: 186
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 140
: LENGTH: 139
: TYPE: PRT
: ORGANISM: Pseudomonas stutzeri
: US-09-848-616-140

```

	Query Match Similarity	22.1%	Score 135.5;	DB 22	Length 139;
	Best Local Similarity	36.0%	Pred. No.	3.2e-07	
Matches	Conservative	10	Mismatches	42	Indels Gaps
Oy	9 RREGSALATINPLKTTVESLSRGIAGSKIR-----ICGTASTATEYTAGVEPDANKG	63			
	: :: :: :	:			
Dd	38 KSNAAAALAETIPRGKEFDAINEGRTPELSTDECYIGITIDTS---SCVDVLDIADDS	94			
Oy	64 VIAVAIEDSGADDITTFOTGTSPPKANRVITLNLTADGWACKSTOPDMPTP	117			
	:::::::::::: :	:			
dD	95 HIECTAKGNAC-----KFDDKITTLNLTADGEWSCAFTDLARKYP	135			

```

1 RESULT: 9
2 US-09-329-884-10
3 ; Sequence 10 Application US/09329884
4 ; GENERAL INFORMATION:
5 ; APPLICANT: Iyvin, Randall T.
6 ; APPLICANT: Hodges, Robert S.
7 ; TITLE OF INVENTION: PSEUDOMONAS TREATMENT
8 ; TITLE OF INVENTION: COMPOSITION AND METHOD
9 ; FILE REFERENCE: 8900-0008, 30
10 ; CURRENT APPLICATION NUMBER: US/09/329,884
11 ; CURRENT FILING DATE: 1999-06-11
12 ; EARLIER APPLICATION NUMBER: US 60/089,155
13 ; EARLIER FILING DATE: 1998-06-12
14 ; NUMBER OF SEQ ID NOS: 22
15 ; SOFTWARE: PASTSEQ for Windows Version 3.0
16 ; SEQ ID NO 10
17 ; LENGTH: 127
18 ; TYPE: PRT
19 ; ORGANISM: Pseudomonas aeruginosa
20 US-09-329-884-10

```

Query Match	21.8%;	Score 133.5;	DB 17;	Length 127;
Best Local Similarity	31.8%;	Pred. No. 4.8e-07;		

Matches 41; Conservative 17; Mismatches 56; Indels 15; Gaps 4;

QY 1 ALEGEFARSGASALATINPLKTTVEESLSRGIAISKIKIGTAA-----STATEYAG 54
 DB 1 ALEGEFARSGASALATINPLKTTVEESLSRGIAISKIKIGTAA-----STATEYAG 54
 QY 55 VEPDANKL-----GVIAVAIEDSGAGDIFTFQGTSSPKNATKVTILNRTADGVWACKST 110
 DB 57 ASQTSQILPTMTGVPQVLDPLTQTITATNGASALISG-QTLTWTVDVNGGWSGSCATT 115
 QY 111 QDPMTFPG 119
 DB 116 VDAKFRPMG 124

RESULT 10
 US-07-809-762A-27

Sequence 27, Application US/07809762A

GENERAL INFORMATION:

APPLICANT: Smith, Alvin W.

TITLE OF INVENTION: ANTIGENIC PREPARATIONS THAT STIMULATE

TITLE OF INVENTION: PRODUCTION OF ANTIBODIES WHICH BIND TO THE PILI OF TYPE IV

TITLE OF INVENTION: PILATED BACTERIA

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSEE: Frederick W. Pepper, Ph.D.

STREET: 11545 W. Bernardo Court, Ste. 302

CITY: San Diego

STATE: CA

COUNTRY: USA

ZIP: 92127

COMPUTER READABLE FORM:

MEDIUM TYPE: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/809/762A

FILING DATE: 19911218

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Pepper Ph.D., Frederick W.

REGISTRATION NUMBER: 31,286

REFERENCE/DOCKET NUMBER: 910260.01

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 451-1120

TELEFAX: (619) 451-9628

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:

LENGTH: 53 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: protein

US-07-809-762A-27

Query Match
 Best Local Similarity 18.6%; Score 114; DB 3; Length 53;
 Matches 23; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 8 ARSEGASALATINPLKTTVEESLSRG 33
 DB 28 ARSEGASALATINPLKTTVEESLSRG 53

RESULT 11

Sequence 6277, Application US/09328352

GENERAL INFORMATION:

APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: G9C99-039A

CURRENT APPLICATION NUMBER: US/09/328,352
 CURRENT FILING DATE: 1999-06-04
 NUMBER OF SEQ ID NOS: 8252
 SEQ ID NO 6277
 LENGTH: 169

QY 8 ARSEGASALATINPLKTTVEESLSRGIAISKI-KIGTTASTATETAGVPPDANKIGVIA 66
 DB 51 ARSQATAGYSEISMRTGDTLNDGTATISLSQVGFATSSGACSA-----IGVTN 102

Query Match
 Best Local Similarity 18.3%; Score 112; DB 17; Length 169;
 Matches 34; Conservative 25; Mismatches 41; Indels 16; Gaps 5;

QY 67 VAIEDSGAGDIFTFQGTSSPKNATKVTILNRTADGVWACK-----STODPMFTPG 119
 DB 103 FGNDGATATATCTLK---GNPKIAGKIISLSRSATGAWTCSTDIATITDE-FLPKG 154

RESULT 12

US-09-329-884-2

Sequence 2, Application US/09329884

GENERAL INFORMATION:

APPLICANT: Irvin, Randall T.

APPLICANT: Hodges, Robert S.

TITLE OF INVENTION: PSEUDOMONAS TREATMENT

FILE REFERENCE: 8900-0008.30

CURRENT APPLICATION NUMBER: US/09/329,884

CURRENT FILING DATE: 1999-06-11

EARLIER APPLICATION NUMBER: US 60/089,155

EARLIER FILING DATE: 1998-06-12

NUMBER OF SEQ ID NOS: 22

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 2

LENGTH: 129

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-329-884-2

Query Match
 Best Local Similarity 17.9%; Score 109.5; DB 17; Length 129;
 Matches 40; Conservative 18; Mismatches 51; Indels 19; Gaps 7;

QY 1 ALEGEFARSGASALATINPLKTTVEESLSRGIAISKIKIGTAASTATTETAGVPPDAN 60
 DB 1 ALEGEFARSGASALATINPLKTTVEESLSRGIAISKIKIGTAASTATTETAGVPPDAN 60

QY 61 KLGVAVAIED-----SGAGDIFTFQ-TGTSSP-KNATVITILNRTADG--VWACKST 110
 DB 52 INGRVAVTIGGTAAASGGCTIVATMAKASDVATPLREKTLTLTLGNADKGSYTWACTSN 111

QY 111 QDPMTFPG 118
 DB 112 ADNRYLPK 119

RESULT 13

US-08-360-107-118

Sequence 118, Application US/08360107

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Peteway, Stephen R.

APPLICANT: Langlois, Alphonse J.


```

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000
1001
1002
1003
1004
1005
1006
1007
1008
1009
1010
1011
1012
1013
1014
1015
1016
1017
1018
1019
1020
1021
1022
1023
1024
1025
1026
1027
1028
1029
1030
1031
1032
1033
1034
1035
1036
1037
1038
1039
1040

```

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,896
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742.
REFERENCE/DOCKET NUMBER: 7872-020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 154 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-470-896-108

Query Match 16.7%; Score 102.5; Db 8; Length 154;
Best Local Similarity 30.2%; Pred. No. 0.0026;
Matches 35; Conservative 18; Mismatches 42; Indels 21; Gaps 5;

Cy 8 ARSECASALATINPLKTTVEESLSRG--IAGS-----KIKIGTASTATETAYAGVDPDA 59
Db 35 ARTQVTRAVSEVSAALKTAESAILEGKEIYSSATPKPDQYDIEFTSTLDD----- 85
60 NKLGVIAVAIEDSGADITTFPQGTSSPNATK--VITLNPRTADGVWCKSTQDP 113
Db 86 -GSGKSQIQVDNDGTVELVATILGKSS-GSAIKGAVITVSRKNDGVWCKITKTP 139

RESULT 15
US-08-471-913-108
Sequence 108, Application US/08471913
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petewave, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
TRANSMISSION
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,913
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.

```

Fri Feb 8 15:44:53 2002

us-09-865-159-6.ram

Page 6

```

: REGISTRATION NUMBER: 30,742
: REFERENCE/DOCKET NUMBER: 7872-030
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 790-9090
: TELEFAX: (212) 869-9741/8864
: TELEX: 66141 PENNIE
: INFORMATION FOR SEQ ID NO: 108:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 154 amino acids
: TYPE: amino acid
: STRANDNESS:
: TOPOLOGY: unknown
: MOLECULE TYPE: protein
US-08-471-913-108

```

Query Match	16.7%	Score 102.5	DB 8	Length 154
Best Local Similarity	30.2%	Pred. No. 0.0026		
Matches 35; Conservative	18;	Mismatches 42;	Indels 21;	Gaps 5;

OY 8 ARSGSALATINPLKPTTVEESLSG--IAG-----KIIGTTATAETAGVPEDA 59
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : :
Db 35 ARQYVRAVSEVSALTAAESAILEGEKVSAFHKDQYIGTESTLLD----- 85

OY 60 NKGVLVALEDSAGADITFTQTGSFRKANR--VTTLNRADGVMAACKSDPP 113
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : :
Db 86 -GSGSKSIQVTDQMGDTVELAVTLKRSS-GSAIKAVATLVSRKNDGWNNKLTKTP 139

Search completed: February 8, 2002, 15:32:39
Job time: 564 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 8, 2002, 15:26:38 ; Search time 37.1 Seconds
(without alignments)
146,409 Million cell updates/sec

Title: US-09-865-159-6

Perfect score: 612
Sequence: 1 ALEGTFFARSEGASALATIN.....GYWACKSTODPMFTPKGSDN 122

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 211743 seqs, 44522877 residues

Total number of hits satisfying chosen parameters: 211743

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending_Patents_AA_New:*
1: /cgn2_6/ptodata/2/paa/US06_PCT_NEW_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	612	100.0	122	5	US-09-865-159-6
2	593.5	97.0	168	5	US-09-865-159-22
3	592	96.7	168	5	US-09-865-159-20
4	325.5	53.2	123	5	US-09-865-159-4
5	307	50.2	169	5	US-09-865-159-14
6	305.5	49.9	169	5	US-09-865-159-12
7	137.5	22.5	127	5	US-09-865-159-8
8	133.5	21.8	127	5	US-09-865-159-10
9	109.5	17.9	129	5	US-09-865-159-2
10	91	14.9	175	5	US-09-865-159-18
11	89.5	14.6	175	5	US-09-865-159-16
12	74.5	12.2	791	6	US-10-015-127-10930
13	74	12.1	183	5	US-09-675-784A-12256
14	74	12.1	666	5	US-09-708-427-30328
15	74	12.1	688	5	US-09-708-427-30327
16	74	12.1	807	5	US-09-708-427-30326
17	73	11.9	473	5	US-09-708-427-54257
18	73	11.9	481	5	US-09-708-427-54256
19	72.5	11.8	690	5	US-09-815-242-12460
20	72.5	11.8	703	5	US-09-815-242-5610
21	72	11.8	1445	6	US-10-015-127-12712
22	71	11.6	781	5	US-09-815-242-11277
23	71	11.6	4315	1	PCT-US01-27760-811
24	71	11.6	4315	1	PCT-US01-27760A-811
25	70	11.4	1597	5	US-09-832-292-35
26	69	11.3	164	5	US-09-815-242-5538

ALIGNMENTS

27	69	11.3	166	5	US-09-815-242-12222	Sequence 12222, A
28	69	11.3	166	5	US-09-815-242-12828	Sequence 12828, A
29	67.5	11.0	218	5	US-09-620-394B-6868	Sequence 6868, A
30	67.5	11.0	218	5	US-09-708-427-23236	Sequence 23236, A
31	67.5	11.0	219	5	US-09-620-394B-6867	Sequence 6867, A
32	67.5	11.0	219	5	US-09-708-427-23235	Sequence 23235, A
33	67.5	11.0	243	5	US-09-708-427-23234	Sequence 23234, A
34	67.5	11.0	271	5	US-09-620-394B-6866	Sequence 6866, A
35	67	10.9	356	5	US-09-897-516-6508	Sequence 6508, A
36	67	10.9	590	5	US-09-708-427-10076	Sequence 10076, A
37	67	10.9	671	5	US-09-708-427-10075	Sequence 10075, A
38	67	10.9	729	5	US-09-708-427-10074	Sequence 10074, A
39	66.5	10.9	302	5	US-09-708-427-55120	Sequence 55120, A
40	66.5	10.9	339	5	US-09-708-427-55119	Sequence 55119, A
41	66.5	10.9	347	5	US-09-708-427-5001	Sequence 5001, A
42	66.5	10.9	388	1	PCT-US01-47182-2	Sequence 2, Appl
43	66.5	10.9	889	5	US-09-952-267-15	Sequence 15, Appl
44	66.5	10.9	889	5	US-09-952-267A-15	Sequence 15, Appl
45	66.5	10.9	1537	5	US-09-801-368-104	Sequence 104, Appl

RESULT 1
US-09-865-159-6
Sequence 6, Application US/09865159
GENERAL INFORMATION:
APPLICANT: Irvin, Randall T.
TITLE OF INVENTION: PSEUDOMONAS TREATMENT
FILE REFERENCE: 8900-0008.30
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329,884
PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 122
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-865-159-6

Query Match 100.0%; Score 612; DB 5; Length 122;
Best Local Similarity 100.0%; Pred. No. 2.4e-54;
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALEGTFFARSEGASALATINPLKTTVEESLSRGISGSKIKITTTASTATETVAGVPPDN 60
DB 1 ALEGTFFARSEGASALATINPLKTTVEESLSRGISGSKIKITTTASTATETVAGVPPDN 60
QY 61 KIGVAVALIEDSGADITFTFOTGTSPPKARKVTLTNTAGCWACKSTODPMFTPKGS 120
DB 61 KIGVAVALIEDSGADITFTFOTGTSPPKARKVTLTNTAGCWACKSTODPMFTPKGS 120
QY 121 DN 122
DB 121 DN 122
RESULT 2
US-09-865-159-22
Sequence 22, Application US/09865159
GENERAL INFORMATION:
APPLICANT: Irvin, Randall T.
TITLE OF INVENTION: PSEUDOMONAS TREATMENT
FILE REFERENCE: 8900-0008.30
CURRENT APPLICATION NUMBER: US/09/865,159

;; CURRENT FILING DATE: 2001-05-24
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329,884
;; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
;; NUMBER OF SEQ ID NOS: 22
;; SOFTWARE: FASTSEQ for Windows Version 3.0
;; SEQ ID NO 22
;; LENGTH: 168
;; TYPE: PRT
;; ORGANISM: Pseudomonas aeruginosa
US-09-865-159-22

Query Match 97.0%; Score 593.5; DB 5; Length 168;
Best Local Similarity 96.8%; Pred. No. 2,6e-52;
Matches 121; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

OY 1 ALE---GTEFARSGASALATINPLKTTVEESLSRGIAGSKIKIGTTASTATETVAGVER 57
||| |
Db 44 ALEGGGGEFARSGASALATINPLKTTVEESLSRGIAGSKIKIGTTASTATETVAGVER 103
OY 58 DANKLGVIAVAIEDSGADITFTFQTGSSPKNATKVTITLNRADGWACKSTODPMT 117
||| |
Db 104 DANKLGVIAVAIEDSGADITFTFQTGSSPKNATKVTITLNRADGWACKSTODPMT 163
OY 118 KGSND 122
||| |
Db 164 KGSND 168

RESULT 3
US-09-865-159-20
; Sequence 20, Application US/09865159
; GENERAL INFORMATION:
; APPLICANT: Irvin, Randall T.
; APPLICANT: Hodges, Robert S.
; TITLE OF INVENTION: PSEUDOMONAS TREATMENT
; FILE REFERENCE: 8900-0008.30
; CURRENT APPLICATION NUMBER: US/09/865,159
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329,884
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-865-159-20

Query Match 96.7%; Score 592; DB 5; Length 168;
Best Local Similarity 99.2%; Pred. No. 3,6e-52;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 GTEFARSGASALATINPLKTTVEESLSRGIAGSKIKIGTTASTATETVAGVERPANKLG 63
||| |
Db 50 GTEFARSGASALATINPLKTTVEESLSRGIAGSKIKIGTTASTATETVAGVERPANKLG 109
OY 64 VIAVAIEDSGADITFTFQTGSSPKNATKVTITLNRADGWACKSTODPMTPKGSND 122
||| |
Db 110 VIAVAIEDSGADITFTFQTGSSPKNATKVTITLNRADGWACKSTODPMTPKGSND 168

RESULT 4
US-09-865-159-4
; Sequence 4, Application US/09865159
; GENERAL INFORMATION:
; APPLICANT: Irvin, Randall T.
; APPLICANT: Hodges, Robert S.
; TITLE OF INVENTION: PSEUDOMONAS TREATMENT
; FILE REFERENCE: 8900-0008.30

;; CURRENT APPLICATION NUMBER: US/09/865,159
;; CURRENT FILING DATE: 2001-05-24
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329,884
;; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
;; NUMBER OF SEQ ID NOS: 22
;; SOFTWARE: FASTSEQ for Windows Version 3.0
;; SEQ ID NO 4
;; LENGTH: 123
;; TYPE: PRT
;; ORGANISM: Pseudomonas aeruginosa
US-09-865-159-4

Query Match 53.2%; Score 325.5; DB 5; Length 123;
Best Local Similarity 60.2%; Pred. No. 1,3e-25;
Matches 74; Conservative 11; Mismatches 31; Indels 7; Gaps 4;

OY 1 ALEGTAFARSGASALATINPLKTTVEESLSRGIAGSKIKIGTTASTAT--ETVAGVERP 58
||| |
Db 1 ALEGTAFARSGASALATINPLKTTVEESLSRGIAGSKIKIGTTASTAT--ETVAGVERP 58
OY 59 ANKLGIVIAVAIEDS--GAGDITFTFQTGSSPKNATKVTITLNR--ADGWACKSTODPMT 116
||| |
Db 58 ANKLGIVIAVAIEDS--GAGDITFTFQTGSSPKNATKVTITLNR--ADGWACKSTODPMT 117
OY 117 PKG 119
||| |
Db 118 PKG 120

RESULT 5
US-09-865-159-14
; Sequence 14, Application US/09865159
; GENERAL INFORMATION:
; APPLICANT: Irvin, Randall T.
; APPLICANT: Hodges, Robert S.
; TITLE OF INVENTION: PSEUDOMONAS TREATMENT
; FILE REFERENCE: 8900-0008.30
; CURRENT APPLICATION NUMBER: US/09/865,159
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329,884
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 169
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-865-159-14

Query Match 50.2%; Score 307; DB 5; Length 169;
Best Local Similarity 57.9%; Pred. No. 1,4e-23;
Matches 73; Conservative 11; Mismatches 32; Indels 10; Gaps 5;

OY 1 ALE---GTEFARSGASALATINPLKTTVEESLSRGIAGSKIKIGTTASTAT--ETVAGV 55
||| |
Db 44 ALEGGGGEFARSGASALATINPLKTTVEESLSRGIAGSKIKIGTTASTAT--ETVAGV 100
OY 56 EPDANKLGVIAVAIEDS--GAGDITFTFQTGSSPKNATKVTITLNR--ADGWACKSTODPMT 113
||| |
Db 101 AADANKLGVIAVAIEDS--GAGDITFTFQTGSSPKNATKVTITLNR--ADGWACKSTODPMT 160
OY 114 MTPKG 119
||| |
Db 161 MTPKG 166

RESULT 6
US-09-865-159-12
; Sequence 12, Application US/09865159
; GENERAL INFORMATION:

```

:
: APPLICANT: Irvin, Randall T.
: APPLICANT: Hodges, Robert S.
: TITLE OF INVENTION: PSEUDOMONAS TREATMENT
: TITLE OF INVENTION: COMPOSITION AND METHOD
: FILE REFERENCE: 8900-0008.30
: CURRENT APPLICATION NUMBER: US/09/865,159
: CURRENT FILING DATE: 2001-05-24
: PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329,884
: PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
: NUMBER OF SEQ ID NOS: 22
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 12
: LENGTH: 169
: TYPE: PRN
: ORGANISM: Pseudomonas aeruginosa
: US-09-865-159-12

```

Query Match	49.9%	Score 305.5;	DB 5,	Length 169;
Best Local Similarity	58.3%	Pred. No. 1.9e-23;		
Matches 70;	Conservative 11;	Mismatches 32;	Indels 7;	Gaps 4;

[illegible]

```

RESULT 7
US-09-865-159-8
: Sequence 8, Application US/09865159
: GENERAL INFORMATION:
: APPLICANT: Irvin, Randall T.
: APPLICANT: Hodges, Robert S.
: TITLE OF INVENTION: PSEUDOMONAS TREATMENT
: TITLE OF INVENTION: COMPOSITION AND METHOD
: FILE REFERENCE: 8900-0008, 30
: CURRENT APPLICATION NUMBER: US/09/865, 159
: CURRENT FILING DATE: 2001-05-24
: PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329, 884
: PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
: NUMBER OF SEQ ID NOS: 22
: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ ID NO 8
: LENGTH: 127
: TYPE: PRT
: ORGANISM: Pseudomonas aeruginosa
US-09-865-159-8

```

Query Match	22.5%	Score 137.5;	DB 5,	Length 127;
Best Local Similarity	34.1%;	Pred. No. 9.5e-07;		
Matches 42;	Conservative 18;	Mismatches 42;	Indels 21;	Gaps 5.

```

QY      1 ALEETEPFRSGASALMTINPLKTTVESISRG--IAGS-----KIKITTSATAEY 52
      1 | | | | | | | | | | : : : : : | | | | | : : : : :
Db      1 ALEGEFAPRTVTHAVSEVSLAKTAAASALILEGKEIYVSMTPKDTQYDIDGFTSTLTD -- 58

QY      53 AGVEPDANKLVIAVAIEDSGAGITTFQGTGTSPPNNAIK--VITLNRADGVMACKST 110
      59 -----GSKSIOIQTVDNKGDELVELVALTGKSS-GSAIKGAVITVSRNDGVMNCKIT 109

```

QY	111 QDP	113
	:	1
Db	110 KTP	112

RESULT 8
US-09-865-159-10
: Sequence 10, Application US/09865159

```

GENERAL INFORMATION:
APPLICANT: Irvlin, Randall T.
APPLICANT: Hodges, Robert S.
TITLE OF INVENTION: PSEUDOMONAS TREATMENT
TITLE OF INVENTION: COMPOSITION AND METHOD
FILE REFERENCE: 8900-0008, 30
CURRENT APPLICATION NUMBER: 09/865,159
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329,884
PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 127
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-865-159-10

```

Query Match	21.8%	Score 133.5	DB 5	Length 127
Best Local Similarity	31.8%	Pred. No. 2.4e-06		
Matches 41	Conservative 17	Mismatches 56	Indels 15	Gaps 4

[illegible]

```
QY 111 QDPMETPKG 119
      | | |
Db 116 VDAKFRPNG 124
```

db 116 VDAKFRPNG 124

RESULT 9
 US-09-865-159-2
 Sequence 2, Application us/09865159
 GENERAL INFORMATION:
 APPLICANT: Irvin, Randall T.
 TITLE OF INVENTION: PSEUDOMONAS TREATMENT
 TITLE OF INVENTION: COMPOSITION AND METHOD
 FILE REFERENCE: 8900-0008, 30
 CURRENT APPLICATION NUMBER: US/09/865,159
 PRIOR FILING DATE: 2001-05-24
 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329,884
 PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
 NUMBER OF SEQ ID NOS: 22
 SOFTWARE: FASTSEQ for Windows Version 3.0
 SEQ ID NO: 2
 LENGTH: 129
 TYPE: PR1
 ORGANISM: Pseudomonas aeruginosa
 US-09-865-159-2

Query Match	17.9%	Score 109.5	DB 5	Length 129
Best Local Similarity	31.2%	Pred. No. 0.00062		
Matches 40	Conservative 18	Mismatches 51	Indels 19	Gaps 7

```
QY      1 ALEGTAFARSEGASALATINPLKTTVEESLRGIAGSKIKIGTASTATETAYAGVEDPAN 60C
          ||||| : : ||| | : : || :|| :||| : :
Db      1 ALEGTFAARAQLSERMTIASGLKTRVSDIFSDD--GS-----CPANTAAAT--AGIEKDTD 51I
```

QY 61 KLGTVAAIED-----SGAGDITTFQ-TGTSSP-KNAKRVITLNRADG--VWACKST 110
| : || | : : : | : || | || |
Db 52 INGRVYAKVTMTGGTAAASGGCTIVATMKASDVAPPLRGKLTLLTCNADKSITYWACTSN 111

QY	111	QDPMEFPK	118
		:	
Db	112	ADNKYLPK	119

```

0Y      4  GTEARSGASALATINLTKTVEESLKGIAKIGTATATETAYAVEPPANKLG  63
      | | | | : : : : | | : : | | : : | | : : | | : : | | : : |
Db      50  GGEARFALSERMTLAKIKTVSDIFSD-----CPANTPAT--AGIEKPDING  100
      | | | | : : : : | | : : | | : : | | : : | | : : | | : : |
0Y      64  VIAAIED-----SGADITFTFPQ--TGTSSP-KNATKYITINRTADG--VWACKSTODP  113
      | | | | : : : : | | : : | | : : | | : : | | : : | | : : |

```

ORGANISM: *Aspergillus fumigatus*.
FEATURE: NAME/KEY: UNSURE
LOCATION: (16)
OTHER INFORMATION: Unknown amino acid
US-09-675-784A-12256

Fri Feb 8 15:44:53 2002

us-09-865-159-6.rapn

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 8, 2002, 15:24:32 ; Search time 67.74 Seconds
(without alignments)
138.874 Million cell updates/sec

Title: US-09-865-159-8

Perfect score: 642
1 ALEGTETARTQVTRAVSEVS.....ITKPTJANKPNYAPNCPS 127

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A.GeneSeq..1101:*

1:	/SIDSB/gcgdata/geneseq/geneseq/AA1980.DAT:*
2:	/SIDSB/gcgdata/geneseq/geneseq/AA1981.DAT:*
3:	/SIDSB/gcgdata/geneseq/geneseq/AA1982.DAT:*
4:	/SIDSB/gcgdata/geneseq/geneseq/AA1983.DAT:*
5:	/SIDSB/gcgdata/geneseq/geneseq/AA1984.DAT:*
6:	/SIDSB/gcgdata/geneseq/geneseq/AA1985.DAT:*
7:	/SIDSB/gcgdata/geneseq/geneseq/AA1986.DAT:*
8:	/SIDSB/gcgdata/geneseq/geneseq/AA1987.DAT:*
9:	/SIDSB/gcgdata/geneseq/geneseq/AA1988.DAT:*
10:	/SIDSB/gcgdata/geneseq/geneseq/AA1989.DAT:*
11:	/SIDSB/gcgdata/geneseq/geneseq/AA1990.DAT:*
12:	/SIDSB/gcgdata/geneseq/geneseq/AA1991.DAT:*
13:	/SIDSB/gcgdata/geneseq/geneseq/AA1992.DAT:*
14:	/SIDSB/gcgdata/geneseq/geneseq/AA1993.DAT:*
15:	/SIDSB/gcgdata/geneseq/geneseq/AA1994.DAT:*
16:	/SIDSB/gcgdata/geneseq/geneseq/AA1995.DAT:*
17:	/SIDSB/gcgdata/geneseq/geneseq/AA1996.DAT:*
18:	/SIDSB/gcgdata/geneseq/geneseq/AA1997.DAT:*
19:	/SIDSB/gcgdata/geneseq/geneseq/AA1998.DAT:*
20:	/SIDSB/gcgdata/geneseq/geneseq/AA1999.DAT:*
21:	/SIDSB/gcgdata/geneseq/geneseq/AA2000.DAT:*
22:	/SIDSB/gcgdata/geneseq/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	642	100.0	127	21	AAV4378	Exemplary truncate
2	186.5	29.0	127	21	AAV4379	Exemplary truncate
3	137.5	21.4	122	21	AAV4377	Exemplary truncate
4	134	20.9	123	21	AAV4376	Exemplary truncate
5	132	20.6	23	13	AAV25904	P.aeruginosa PI pil
6	132	20.6	23	13	AAV25904	P.aeruginosa PI pil
7	128	19.9	22	17	AAV25905	P.aeruginosa PI pil
8	119	18.5	168	21	AAV4385	P.aeruginosa E coli
9	117.5	18.3	168	21	AAV4384	P.aeruginosa E coli
10	115.5	18.0	169	21	AAV4381	P.aeruginosa E coli
11	115	17.9	19	11	AAV4381	P.aeruginosa E coli

12	115	17.9	19	21	AAV4363	C-terminal cell su
13	114	17.8	169	21	AAV4380	P.aeruginosa H co
14	106	16.5	24	18	AAV19279	Pseudomonas aerugi
15	101.5	15.8	129	21	AAV4375	Exemplary truncate
16	98	15.3	17	18	AAV19278	Pseudomonas aerugi
17	98	15.3	23	13	AAV25907	P.aeruginosa TB0U1
18	90	14.0	22	13	AAV25906	P.aeruginosa TB0U1
19	90	14.0	22	17	AAV25906	P.aeruginosa TB0U1
20	87	13.6	19	11	AAV25905	P.aeruginosa TB0U1
21	87	13.6	19	21	AAV4365	P.aeruginosa TB0U1
22	87	13.6	23	13	AAV25905	P.aeruginosa TB0U1
23	85	13.2	22	17	AAV25905	P.aeruginosa TB0U1
24	84	13.1	82	14	AAV25905	P.aeruginosa TB0U1
25	83	12.9	19	11	AAV25905	P.aeruginosa TB0U1
26	83	12.9	19	21	AAV4363	P.aeruginosa TB0U1
27	83	12.9	175	21	AAV4363	P.aeruginosa TB0U1
28	83	12.9	409	21	AAV4363	P.aeruginosa TB0U1
29	81.5	12.7	175	21	AAV4382	P.aeruginosa TB0U1
30	80	12.5	69	21	AAV4382	P.aeruginosa TB0U1
31	79.5	12.4	273	12	AAV4382	P.aeruginosa TB0U1
32	79.5	12.4	287	14	AAV4382	P.aeruginosa TB0U1
33	79.5	12.4	338	14	AAV4382	P.aeruginosa TB0U1
34	79	12.3	934	18	AAV4382	P.aeruginosa TB0U1
35	79	12.3	934	18	AAV4382	P.aeruginosa TB0U1
36	78.5	12.2	150	20	AAV4382	P.aeruginosa TB0U1
37	78.5	12.2	904	21	AAV4382	P.aeruginosa TB0U1
38	78.5	12.2	935	15	AAV4382	P.aeruginosa TB0U1
39	78.5	12.2	935	15	AAV4382	P.aeruginosa TB0U1
40	77	12.0	593	11	AAV4382	P.aeruginosa TB0U1
41	76.5	11.9	273	16	AAV4382	P.aeruginosa TB0U1
42	76.5	11.9	343	21	AAV4382	P.aeruginosa TB0U1
43	76.5	11.9	343	21	AAV4382	P.aeruginosa TB0U1
44	76.5	11.9	386	19	AAV4382	P.aeruginosa TB0U1
45	76.5	11.9	393	19	AAV4382	P.aeruginosa TB0U1

ALIGNMENTS

RESULT 1
AAV4378 standard; Protein: 127 AA.

ID	AAV4378	standard	Protein: 127 AA
XX	AAV4378;		
AC	14-MAR-2000	(first entry)	
DT	Exemplary truncated P. aeruginosa PI pilin protein.		
XX	Modified PI pilin protein; alpha-helical forming portion:		
KW	Pseudomonas infection; cystic fibrosis; neutropenia.		
KW	Pseudomonas aeruginosa.		
OS	W09965511-AZ.		
PN	23-DEC-1999.		
XX	11-JUN-1999;	99WC-CA00554.	
PF	12-JUN-1998;	98US-0089155.	
XX	(UTAL-) UNIV ALBERTA.		
PA	Hodges RS, Irvin RT;		
XX	WPI: 2000-106013/09.		
DR	N-PSDB: AAV229537.		
XX	Composition for treating or preventing Pseudomonas aeruginosa infection		
PT	comprising pilin protein that can not self-assemble		
XX	Claim 9; Fig 1D; 32pp; English.		

XX The present sequence is the modified P1 pilin protein from
CC P.aeruginosa. The N-terminal peptide region preferably lacks the first
CC 15-40 residues of native P.aeruginosa. Modified pilin proteins are
CC prepared by PCR amplification of pilin coding sequences using primers
CC that effect the desired deletion, modification or insertion of a coiled-
CC coil moiety in the coding sequences. The modified protein thus lacks a
CC critical alpha-helical forming portion. This prevents oligomerisation of
CC pilin protein necessary for attachment to the host cell during infection
CC The ligated plasmid DNA was transformed into an expression host. The
CC modified pilin protein is useful in treatment and prophylaxis for
CC individuals at risk of Pseudomonas infection, e.g. cystic fibrosis
CC patients, burn patients, and severe neutropenic patients.
XX
50 Sequence 127 AA;

Query Match	100.0%	Score 642:	DB 21:	Length 127:
Best Local Similarity	100.0%	Pred. No. 4.2e-61:		
Matches 127; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0
QY	1	ALEGTETARTQYTRAVSEVSAIKLTAAESAILGKEIKVISATPKPDYDIDGTFESTLLDGS	60	
Db	1	alegrefartqytravsevsalktaaesallegkeltvssalpkdtydldgftestlldgs	60	
QY	61	GKSQIQVDDNKGIVELVATLTKSSGSAIKGAVIYSRKNDGVWNCITTKTPAMKPNTA	120	
Db	61	gksiqivdndkgiveltvialtkssgsaikgavilvsirkndgvwncklktplawkpnaya	120	
QY	121	PANCPNS	127	
Db	121	pancpns	127	

	RESULT	2
AAAY44379	ID	AAI44379 standard; Protein: 127 AA.
XX		
AC	AAY44379;	
XX		
DT	14-MAR-2000	(first entry)
XX		
DE	Exemplary truncated P. aeruginosa KB7 pilin protein.	
KW	Modified KB7 pilin protein; alpha-helical forming portion;	
RW	Pseudomonas infection; cystic fibrosis; neutropenia.	
XX		
OS	Pseudomonas aeruginosa.	
XX		
PN	WO9965511-A2.	
XX		
PD	23-DEC-1999.	
XX		
PF	11-JUN-1999;	99WO-CA0054.
XX		
PR	12-JUN-1998;	98US-0089155.
XX		
PA	(UYAL-) UNIV ALBERTA.	
PI	Hodges RS,	Irvin RT;
XX		
DR	WI: 2000-106013/09.	
DR	N-PSTDB:	MAZ29538.
PT	Composition for treating or preventing Pseudomonas aeruginosa infection	
PT	comprising pilin protein that can not self-assemble -	
PS	Claim 9;	Fig 1E; 32pp; English.
CC	The present sequence is the modified KB7 pilin protein from	
CC	P. aeruginosa. The N-terminal peptide region preferably lacks the first	
CC	15-40 residues of native P.aeruginosa. Modified pilin proteins are	
CC	prepared by PCR amplification of pilin coding sequences using primers	

CC that effect the desired deletion, modification or insertion of a collagen
CC coil moiety in the coding sequences. The modified protein thus lacks a
CC critical alpha-helical forming portion. This prevents oligomerisation of
CC p11n protein necessary for attachment to the host cell during infection
CC The ligated plasmid DNA was transformed into an expression host. The
CC modified p11n protein is useful in treatment and prophylaxis for
CC individuals at risk of Pseudomonas infection, e.g. cystic fibrosis
CC patients, burn patients, and severe neutropenic patients.

```

Query Match      29.0%; Score 186.5; DB 21; Length 127;
Best Local Similarity 35.4%; Pred. No. 2.4e-12;
Matches 45; Conservative 25; Mismatches 44; Indels 13; Gaps 3.

QY 1 ALEGTGFARTOVTRAIVSEVSAIKTAAESALKEGKEIVSAMPKRDYDIDGETESTLLDGS 60
   |||||:-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:
pB 1 alegetgfartovtraivsevsaiiktaveaalqdgqrlavtga---gqcpgatgsslltga 57
   |||||:-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:

QY 61 GKSQ-----IDVTDNKDGTVELVATLTKSSSSAIKGAIVITYSRKDKGVWNCKITFT 111
   :|:-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:
pB 58 sqtsqldplntgvpvpldltqtftlialtfggaasaaatgqltwtlvrdvngwsc-atlv 116
   :|:-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:

QY 112 PTAKPN 118
   :|:-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:
pB 117 dakirpn 123
   :|:-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:

```

RESULT 3
AAV44377
ID AAV44377 standard; Protein; 122 AA.
XX
AC AAV44377:
XX
DT 14-MAR-2000 (first entry)
XX
DE Exemplary truncated *P. aeruginosa* PAO pilin protein.
XX
KW Modified PAO pilin protein; alpha-helical forming portion;
KM Pseudomonas infection; cystic fibrosis; neutropenia.
XX
OS Pseudomonas aeruginosa.
XX
PN WO965511-A2.
XX
PD 23-DEC-1999.
XX
PF 11-JUN-1999; 99WO-CA00554.
XX
PR 12-JUN-1998; 98US-0089155.
XX
PA (UYAL-) UNIV ALBERTA.
XX
PI Hodges RS, Irvln RT;
XX
DR WPI: 2000-106013/09.
XX
PS N-PSDB; AAZ29536.
XX
PT Composition for treating or preventing Pseudomonas aeruginosa infection
XX comprising pilin protein that can not self-assemble -
XX
XX Claim 9; Fig 1C; 32pp; English.
XX
XX The present sequence is the modified PAO pilin protein from
XX *P. aeruginosa*. The N-terminal peptide region preferably lacks the first
XX 15-40 residues of native *P. aeruginosa*. Modified pilin proteins are
XX prepared by PCR amplification of pilin coding sequences using primers
XX that effect the desired deletion, modification or insertion of a coiled-
XX coil moiety in the coding sequences. The modified protein thus lacks a
XX critical alpha-helical forming portion. This prevents oligomerisation of
XX pilin protein necessary for attachment to the host cell during infection
XX The ligated plasmid DNA was transformed into an expression host. The

ID AAY49369 standard; peptide; 23 AA.
 XX
 AC AAY49369;
 XX
 DT 14-MAR-2000 (first entry)
 XX
 DE Cell surface binding domain from P. aeruginosa pilin strain Pl.
 XX
 KW Vaccine; P. aeruginosa; pilin; Pseudomonas infection; antibacterial;
 KM cell surface binding domain.
 XX
 OS Pseudomonas aeruginosa.
 XX
 PN WO957142-A2.
 XX
 PD 11-NOV-1999.
 XX
 PF 06-MAY-1999; 99WO-CA00366.
 XX
 PR 06-MAY-1998; 98US-0084444.
 XX
 PA (UYAL-) UNIV ALBERTA.
 XX
 PI Hodges RS, Irvin RT, Cachia PJ;
 DR WPI: 2000-072227/06.
 XX
 PT Novel vaccine used to prevent Pseudomonas aeruginosa infection -
 XX
 PS Disclosure; Fig 11; 21pp; English.
 XX
 CC The invention provides a peptide vaccine against P. aeruginosa that
 CC comprises a pilin peptide conjugated to a carrier protein. The pilin
 CC peptide has one of the four sequences selected from AAY49352-355. The
 CC vaccine is used to prevent Pseudomonas infections. The present sequence
 CC represents a cell surface binding domain from P. aeruginosa pilin strain
 CC Pl.
 CC
 SQ Sequence 23 AA;

Query Match 20.6%; Score 132; DB 21; Length 23;
 Best Local Similarity 95.7%; Pred. No. 1.5e-07;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 105 NCKITKTPAMKPNYPANCPNS 127
 DB 1 nckitktpamkpnypanpcps 23

RESULT 7
 AAR86705
 ID AAR86705 standard; peptide; 22 AA.
 XX
 AC AAR86705;
 XX
 DT 26-JUN-1996 (first entry)
 XX
 DE Pilin derived peptide, Pl.
 XX
 KW Epitope; exoenzyme; ExoS; enzymatic/cytotoxic protein; PK99H; MCAL;
 KW P. aeruginosa; adhesin; monoclonal antibody; buccal epithelial cell;
 KW cell surface receptor; adhesion domain; pilin protein; vaccine;
 KW immunisation; infection; targeted drug delivery; carcinoma;
 KM pulmonary epithelial cell.
 XX
 OS Pseudomonas aeruginosa.
 XX
 PN US5468484-A.
 XX
 PD 21-NOV-1995.
 XX
 PF 25-JUN-1991; 91US-0721759.

XX
 PR 28-JUN-1993; 93US-0084739.
 PR 25-JUN-1991; 91US-0721759.
 XX
 PA (SPIIS-) SPI SYNTHETIC PEPTIDES INC.
 XX
 PI Hodges RS, Irvin RT, Paranchych W, Sokol PA, Woods DE;
 DR WPI: 1996-010050/01.
 XX
 PT Preventing P. aeruginosa infections by passive immunisation - using
 PT monoclonal antibody reactive with exos and pilin peptide epitope(s)
 XX
 PS Claim 1; Column 31-32; 26pp; English.
 XX
 CC The sequences given in AAR86702-08 are peptides which have the same
 CC immunoreactivity as the peptide sequence given in AAR86701. These
 CC peptides are derived from the P. aeruginosa pilin protein. The peptide
 CC of the invention is derived from the exoenzyme, ExoS. ExoS is an
 CC enzymatic/cytotoxic protein present on the surface of P. aeruginosa
 CC cells. It is also an adhesin. It demonstrates immunospecific binding
 CC to monoclonal antibodies PK99H and MCAL. The ExoS derived peptide has
 CC the ability to block binding of P. aeruginosa to buccal epithelial cells
 CC by blocking a cell surface receptor. It is homologous to known adhesion
 CC domains in the P. aeruginosa pilin protein, esp. the region 131-143.
 CC These peptides may be used in vaccines to provide active immunisation
 CC against infection by P. aeruginosa or related organisms. They can also
 CC be used for targeted drug delivery to pulmonary epithelial cells, e.g.
 CC chemotherapeutic agents.
 CC
 SQ Sequence 22 AA;

Query Match 19.9%; Score 128; DB 17; Length 22;
 Best Local Similarity 100.0%; Pred. No. 3.8e-07;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 NCKITKTPAMKPNYPANCP 125
 DB 1 nckitktpamkpnypanpcp 21

RESULT 8
 AAY44385
 ID AAY44385 standard; Protein; 168 AA.
 XX
 AC AAY44385;
 XX
 DT 14-MAR-2000 (first entry)
 XX
 DE P. aeruginosa E coil-truncated PAO pilin protein.
 XX
 KW Modified PAO pilin protein; alpha-helical forming portion; E coil;
 KW Exemplary coil; coiled coil heterodimer; host cell-receptor site;
 KW Pseudomonas infection; cystic fibrosis; neutropenia.
 XX
 OS Pseudomonas aeruginosa.
 XX
 PN WO965511-A2.
 XX
 PD 23-DEC-1999.
 XX
 PF 11-JUN-1999; 99WO-CA00554.
 XX
 PR 12-JUN-1998; 98US-0089155.
 XX
 PA (UYAL-) UNIV ALBERTA.
 XX
 PI Hodges RS, Irvin RT;
 DR WPI: 2000-106013/09.
 DR N-PSDB; AAZ29544.

XX Composition for treating or preventing *Pseudomonas aeruginosa* infection
PT comprising pilin protein that can not self-assemble -
XX
PS Claim 1; Fig 5B; 32pp; English.
XX
CC The present sequence encodes E coil truncated PAO pilin protein from
CC *P. aeruginosa*. The first 15-40 residues of the N-terminal peptide region
CC is replaced by a peptide segment capable of forming a coiled-coil
CC heterodimer with an oppositely charged peptide segment which can form
CC dimeric structures. These proteins are less inflammatory due to reduced
CC degree of mobilisation of host-cell receptor sites. This prevents
CC oligomerisation of pilin protein necessary for attachment to the host
CC cell during infection. The modified pilin protein is useful in treatment
CC and prophylaxis for individuals at risk of *Pseudomonas* infection,
CC e.g. cystic fibrosis patients, burn patients, and severe neutropenic
CC patients.
CC
CC Sequence 168 AA;
SO

Query Match 18.5%; Score 119; DB 21; Length 168;
Best Local Similarity 32.5%; Pred. No. 6.1e-05;
Matches 41; Conservative 18; Mismatches 43; Indels 24; Gaps 6;

OY 1 ALE---GTEFARTQVTRAVSEVSAIKTAESAILEGKEIVSSATPKDQYDIGTFESTLL 57
| | | | | : : : : : | : : : : : | : : : : : | : : : : :
Db 44 alekgggelfarsegasalaclnplktveeslsrg--laqs-----kikigtastat 95
OY 58 D-----GSGKSOIQVTDNKDGIVELVATLGKSS-GSAIKGAVITVRKNDGVWNC 106
:
Db 96 etyggvepdanklgivavaledsgagdlftfgtgspskhatk--vltlnrtadgyvac 153
OY 107 KITKTP 112
| : : : :
Db 154 kstqdp 159

RESULT 9
AA44384
ID AA44384 standard; Protein; 168 AA.
XX
AC AA44384;
XX
DT 14-MAR-2000 (first entry)
XX
DE *P. aeruginosa* H coil-truncated PAO pilin protein.
XX
KW Modified PAO pilin protein; alpha-helical forming portion;
KW coiled coil homodimer; host cell-receptor site; *Pseudomonas* infection;
KW cystic fibrosis; neutropenia.
XX
OS *Pseudomonas aeruginosa*.
XX
PN W09965511-A2.
XX
PD 23-DEC-1999.
XX
PF 11-JUN-1999; 99WO-CA00554.
XX
PR 12-JUN-1998; 98US-0089155.
XX
PA (UYAL-) UNIV ALBERTA.
XX
PI Hodges RS, Irvin RT;
XX
DR WPI: 2000-106013/09.
DR N-PSDB: AA229543.
XX
PT Composition for treating or preventing *Pseudomonas aeruginosa* infection
PT comprising pilin protein that can not self-assemble -
XX
PS Claim 1; Fig 5A; 32pp; English.

XX
CC The present sequence is the H coil truncated PAO pilin protein from
CC *P. aeruginosa*. The first 15-40 residues of the N-terminal peptide region
CC is replaced by a peptide segment capable of forming a coiled-coil
CC homodimer with an identical peptide segment which can form dimeric
CC structures. These proteins are less inflammatory due to reduced degree of
CC mobilisation of host-cell receptor sites. This prevents oligomerisation
CC of pilin protein necessary for attachment to the host cell during
CC infection. The modified pilin protein is useful in treatment and
CC prophylaxis for individuals at risk of *Pseudomonas* infection,
CC e.g. cystic fibrosis patients, burn patients, and severe neutropenic
CC patients.
CC
CC Sequence 168 AA;
SO

Query Match 18.3%; Score 117.5; DB 21; Length 168;
Best Local Similarity 31.7%; Pred. No. 8.8e-05;
Matches 38; Conservative 18; Mismatches 43; Indels 21; Gaps 5;

OY 4 GTEFARTQVTRAVSEVSAIKTAESAILEGKEIVSSATPKDQYDIGTFESTILD----- 58
| | | | | : : : : : | : : : : : | : : : : : | : : : : :
Db 50 ggetarfsgasalaclnplktveeslsrg--laqs-----kikigtastatetyagv 101
OY 59 -----GSGKSOIQVTDNKDGIVELVATLGKSS-GSAIKGAVITVRKNDGVWNCKITKTP 112
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db 102 epdanklgivavaledsgagdlftfgtgspskhatk--vltlnrtadgyvacsktqdp 159

RESULT 10
AA44381
ID AA44381 standard; Protein; 169 AA.
XX
AC AA44381;
XX
DT 14-MAR-2000 (first entry)
XX
DE *P. aeruginosa* E coil-truncated PAK pilin protein.
XX
KW Modified PAK pilin protein; alpha-helical forming portion; E coil;
KW Exemplary coil; coiled coil heterodimer; host cell-receptor site;
KW *Pseudomonas* infection; cystic fibrosis; neutropenia.
XX
OS *Pseudomonas aeruginosa*.
XX
PN W09965511-A2.
XX
PD 23-DEC-1999.
XX
PF 11-JUN-1999; 99WO-CA00554.
XX
PR 12-JUN-1998; 98US-0089155.
XX
PA (UYAL-) UNIV ALBERTA.
XX
PI Hodges RS, Irvin RT;
XX
DR WPI: 2000-106013/09.
DR N-PSDB: AA229540.
XX
PT Composition for treating or preventing *Pseudomonas aeruginosa* infection
PT comprising pilin protein that can not self-assemble -
XX
PS Claim 1; Fig 3B; 32pp; English.

The present sequence encodes E coil truncated PAK pilin protein from
P. aeruginosa. The first 15-40 residues of the N-terminal peptide region
is replaced by a peptide segment capable of forming a coiled-coil
heterodimer with an oppositely charged peptide segment which can form
dimeric structures. These proteins are less inflammatory due to reduced
degree of mobilisation of host-cell receptor sites. This prevents
oligomerisation of pilin protein necessary for attachment to the host
cell during infection. The modified pilin protein is useful in treatment

	Matches	19, Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	106	CKIKPTAKMPNYPANNC	124						
db	1	CKIKPTAKMPNYPANNC	19						

RESULT	12	.
AYY49363		
ID	AYY49363	standard: peptide: 19 AA

Strain	Cell surface binding domain from <i>P. aeruginosa</i> strain PI
De	C-terminal
XX	cell surface binding domain from <i>P. aeruginosa</i> strain PI
Vaccine; P. aeruginosa: p11n	<i>Pseudomonas</i> infection; antibacterial
FW	

Pseud

PN W09957142-A2.

PD 11-NOV-1999

06-MAY-1999:

PR 06-MAY-1998; 98US-0084444.

PA (UYAL-) UNIV ALBERTA

PI Hodges BS, Trvin RT, Cackbia PT.

WPT: 2000-072227/06

Novel vaccine used +

PS Disclosure: Fida T

The invention pro

comprises a peptide has one of

cc represents a cell

Sequence 19 AA:

Best Local Similarity

Matches 19; Consequence

106 СИТКПТАВКЕ

```

Db          1 CkltKtPawknpyapanc 19
|||||
RESULT      13
ID           AAY44380
              AAY44380 standard; Protein; 169 AA.
XX
AC
XX
XX
AAY44380;
14-MAR-2000 (first entry)
P. aeruginosa H coil-truncated pax pilin protein
```

Modified PAK pilli

CYCLIC DIOSIS;

Pseudomonas aeruginosa

XX	PN	WO965511-A2.
XX	PD	23-DEC-1999.
XX	PF	11-JUN-1999; 99WO-CA00554.
XX	PR	12-JUN-1998; 98US-0089155.
XX	PA	(UYAL-) UNIV ALBERTA.
XX	PI	Hodges RS, Irvin RT;
XX	DR	WPI: 2000-106013/09.
XX	DR	N-PSDB; AA2293539.
XX	PT	Composition for treating or preventing Pseudomonas aeruginosa infection
XX	PT	comprising pilin protein that can not self-assemble -
XX	PS	Claim 1, Fig 3A; 32pp; English.
XX	CC	The present sequence is the H coil truncated PAK pilin protein from
XX	CC	<i>P. aeruginosa</i> . The first 15-40 residues of the N-terminal peptide region
XX	CC	is replaced by a peptide segment capable of forming a coiled-coil
XX	CC	homodimer with an identical peptide segment which can form dimeric
XX	CC	structures. These proteins are less inflammatory due to reduced degree of
XX	CC	mobilitisation of host-cell receptor sites. This prevents oligomerisation
XX	CC	of pilin protein necessary for attachment to the host cell during
XX	CC	infection. The modified pilin protein is useful in treatment and
XX	CC	prophylaxis for individuals at risk of <i>Pseudomonas</i> infection,
XX	CC	e.g. cystic fibrosis patients, burn patients, and severe neutropenic
XX	CC	patients.
XX	Sequence	169 AA;

```

XX      (USSA ) USAHRMRC US ARMY MEDICAL RES MATERIAL COMMAND.
XX
PI      Castric P, Cross A, Sadoff J;
XX
DR      WPI: 1997-351043/32.
XX
XX      DNA encoding Pseudomonas aeruginosa pilQ - which glycosylates pilin,
PT      useful to develop products to diagnose and in vaccines for
PT      Gram-negative bacterial infections
XX
PS      Example 10; Page 43; 60pp; English.
XX
CC      This peptide sequence comprises a surface peptide epitope of
CC      Pseudomonas aeruginosa group 1 strain 1244 pilin. It was
CC      identified using the Geysen tethered peptide pin assay in which
CC      tethered peptides (12-mers, 1 residue overlap per peptide)
CC      representing the entire pilin primary structure were probed with
CC      mouse anti-native 1244 pilus polyclonal sera. The peptide is a
CC      potential protective epitope of use in vaccine design. A claimed
CC      multivalent vaccine against gram-negative bacterial (Gnb)
CC      infections comprises a group of pilin-glycan conjugates of
CC      different Gnb strains or species.
XX
XX      Sequence      24 AA:
XX      1
XX
XX      Query Match      16.5%; Score 106; DB 18; Length 24;
XX      Best Local Similarity 100.0%; Pred. No. 9,7e-05;
XX      Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      14 RAVSEVSAALKTAESAIILEGKEIV 37
XX      |||||||||||||||||||
XX      1 RAVSEVSAALKtaesaIIegkeiv 24

```

	Query Match	17.8%	Score 114	DB 21	Length 169
	Similarity	32.4%	Pred. NO. 0.00021		
	Matches	36	Conservative 19	Mismatches 4	Indels 14
				Gaps 6	
Qy	4	GTEFARTQTVRAVSEVALKTAFAESAILLEGKEIVS----	SATPKDQYDIDGFEFSTLLD	58	
Db	50	ggfeifrsqgaalavmpklktveealstgrwsvksqctgdedtkkveplgyaadanl	--	107	
Qy	59	GSQSQIQVTVNKNKDET--VELVATLQKSSGSAIKCAVITVSR-KNDGVVNC		106	
Db	108	--gtlaak-pdpadgtaadtltltfmg--gaqpnknkikiltlttaadgllkc		154	

XX		RESULT 14
AA	AM19279	
ID	AA19279 standard; Peptide: 24 AA.	
XX		
AC	AA19279;	
XX		
DT	30-DEC-1997 (first entry)	
XX		
DE	Pseudomonas aeruginosa pilus surface peptide epitope.	
XX		
KW	pilA; pilin; glycosylation; Gram-negative bacterium; infection; diagnosis; vaccine; O antigen; pILO.	
XX		
OS	Pseudomonas aeruginosa strain 1244.	
XX		
EN	WO9723600-A1.	
XX		
PD	03-JUL-1997.	
XX		
PF	19-DEC-1996; 96WO-US19747.	
XX		
PR	18-DEC-1996; 96US-0768176.	
FR	22-DEC-1995; 95US-0009190.	
XX		

	RESULT	15
XX	AAAY44375	
ID	AAI44375 standard; Protein: 129 AA.	
XX		
AC	AAV44375;	
XX		
DY	14-MAR-2000 (first entry)	
DE	Exemplary truncated P. aeruginosa K122 pilin protein.	
XX		
KW	Modified K122 pilin protein; alpha-helical forming portion;	
RN	Pseudomonas infection; cystic fibrosis; neutropenia.	
OS	Pseudomonas aeruginosa.	
PN	WO965511-A2.	
PD	23-DEC-1999.	
PF	11-JUN-1999; 99WO-CA00554.	
PR	12-JUN-1998; 98US-0089155.	
PA	(UTAL-) UNIT ALBERTA.	
PI	Hodges RS, Irvin RT;	
DR	N-PSTDB; AAZ29534.	
PT	Composition for treating or preventing Pseudomonas aeruginosa infection comprising pilin protein that can self-assemble -	
PS	Claim 9; Fig 1A; 32pp; English.	
CC	The present sequence is the modified K122 pilin protein from strain P.aeruginosa. The N-terminal 1-28 residues are deleted from K122 strain pilin protein. The modified protein thus lacks a critical alpha-helical CC	

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 8, 2002, 15:25:56 ; Search time 37.87 Seconds
(without alignments)
255.457 Million cell updates/sec

Title: US-09-865-159-8

Perfect score: 642

Sequence: 1 ALBGEFFARQVTRAVSEVS.....ITKPTAMKPNVAPANCPS 127

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008

Listing first 45 summaries

Database :

1: PIR68:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	601	93.6	154	2 B31105	fimbrial protein P
2	597	93.0	154	2 S04440	fimbrial protein -
3	204	31.8	164	2 A42460	fimbrial protein Q
4	189	29.4	157	2 A24434	beta fimbrial prot
5	181	28.2	156	2 A41490	pilin precursor -
6	167.5	26.1	155	2 JL0071	alpha-pilin - Mora
7	166	25.9	159	2 A47699	type 4 pilin - Elk
8	160.5	25.0	156	2 S15266	fima protein - Dic
9	160.5	25.0	157	2 A46566	pilin precursor -
10	151	23.5	158	2 A55851	prepilin - Moraxel
11	133.5	20.8	160	2 A37167	pilin precursor -
12	132.5	20.6	159	2 B47699	N-methylphenylalan
13	132	20.6	156	2 S15267	fima protein - Dic
14	129	20.1	136	2 S52692	pilin precursor -
15	121	18.8	150	2 A43504	pilin precursor -
16	117	18.2	150	2 B24603	fimbrial protein -
17	112	17.4	149	2 A25023	type 4 fimbrial pr
18	108.5	16.9	148	2 C82544	fimbrial protein X
19	102	15.9	135	2 S52693	fimbriillin - Xanth
20	99	15.4	150	1 YQPSPA	fimbrial protein P
21	98	15.3	159	1 YQBDZ	fimbrial protein f
22	96	15.0	136	2 D36961	pilin pila precurs
23	95	14.8	159	1 YQBRHZ	fimbrial protein f
24	85	13.2	692	1 S46853	phosphotransferase
25	85	13.2	1051	2 T48933	WD repeat domain P
26	84.5	13.1	675	1 S46952	phosphotransferase
27	84	13.0	263	1 I41172	cipe protein - Esc
28	83.5	12.9	273	2 S71541	outer surface prot
29	83	12.9	525	2 T23304	hypothetical prote

30	83	12.9	534	2 T23305	hypothetical prote
31	82.5	12.9	241	2 D35270	spiralin precursor
32	81	12.6	507	2 S05542	hypothetical prote
33	80.5	12.5	277	2 H86589	hypothetical prote
34	80.5	12.5	277	2 C72033	hypothetical prote
35	79.5	12.4	273	2 I40102	outer surface prot
36	79.5	12.4	273	2 I40099	outer surface prot
37	79.5	12.4	273	2 I40097	outer surface prot
38	79.5	12.4	273	2 S23112	outer surface prot
39	79.5	12.4	273	2 S71531	outer surface prot
40	79.5	12.4	1050	3 JC7578	endo-1,4-beta-xyla
41	79	12.3	934	2 C86045	intimin adherence
42	78.5	12.2	935	1 I41193	outer membrane pro
43	77	12.0	274	2 S71526	outer surface prot
44	77	12.0	494	2 S07276	flagellin H-1A - S
45	77	12.0	744	2 T45943	hypothetical prote

ALIGNMENTS

```
RESULT 1
B31105
fimbrial protein precursor - Pseudomonas aeruginosa (strain P1)
C:Species: Pseudomonas aeruginosa
C>Date: 31-Mar-1990 #sequence.revision 31-Mar-1990 #text.change 08-Oct-1999
C:Accession: B31105
R:Pasloske, B.L.; Sastry, P.A.; Finlay, B.B.; Paranchych, W.
J. Bacteriol. 170, 3738-3741, 1988
A:Title: Two unusual pilin sequences from different isolates of Pseudomonas aerugino
A:Reference number: A91879; MUID:88298689
A:Accession: B31105
A:Molecule type: DNA
A:Residues: 1-154 <PAS>
A:Cross-references: GB:M21652; NID:g151471; PIDN:AAC63060.1; PID:g151472
C:Superfamily: gonococcal fimbrial protein
F:1-6/Domain: signal sequence #status predicted <SIG>
F:7-154/Product: fimbrial protein #status predicted <MAT>

Query Match          93.6%; Score 601; DB 2; Length 154;
Best Local Similarity 99.2%; Pred. No. 5.3e-47;
Matches 119; Conservative 0; Mismatches 1; Indels 0;

OY 8 ARTQVTRAVSEVSALKTAAESAILGKEIVSAPPKDTQYDIGFTESFLDGGSGKSQIQY 67
|||||
Db 35 ARTQVTRAVSEVSALKTAAESAILGKEIVSAPPKDTQYDIGFTESFLDGGSGKSQIQY 94
|||||

OY 68 TDNKGIVELVATLGKSSGSAIKGAVTVSRKNDGVMWCKITTKPTAMKPNVAPANCPS 127
|||||
Db 95 TDNKGIVELVATLGKSSGSAIKGAVTVSRKNDGVMWCKITTKPTAMKPNVAPANCPS 154
|||||

RESULT 2
S04440
fimbrial protein - Pseudomonas aeruginosa (strain 1244)
N:Alternate names: pilin
C:Species: Pseudomonas aeruginosa
C>Date: 07-Jun-1990 #sequence.revision 07-Jun-1990 #text.change 26-Aug-1999
R:Castro, P.A.; Sidberry, H.F.; Sadoff, J.C.
Mol. Gen. Genet. 216, 75-80, 1989
A:Title: Cloning and sequencing of the Pseudomonas aeruginosa 1244 pilin structural
A:Reference number: S04440; MUID:89281493
A:Accession: S04440
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-154 <CAS>
C:Superfamily: gonococcal fimbrial protein

Query Match          93.0%; Score 597; DB 2; Length 154;
Best Local Similarity 98.3%; Pred. No. 1.2e-46;
```

Matches 118; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 ARTQVTRAVSEVSAALKTAESAILEGKEIYSSATPKDYOYDIGFTESTLLDGSQSIQ 67
 Db 35 ARTQVTRAVSEVSAALKTAESAILEGKEIYSSATPKDYOYDIGFTESTLLDGSQSIQ 94
 QY 68 TDNRDGVVELVATILGKSSGSAIKGAVITVSRKNDGVNCKITKTPAMKPNYAPANCPS 127
 Db 95 TDNRDGVVELVATILGKSSGSAIKGAVITVSRKNDGVNCKITKTPAMKPNYAPANCPS 154

RESULT 3

A42460

fimbrial protein Q - Moraxella lacunata (ATCC 17956) plasmid pMXL1

C:Species: Moraxella lacunata

C:Date: 24-Jul-1992 #sequence_revision 24-Jul-1992 #text_change 29-Jan-1999

C:Accession: A42460

R:Roza, F.W.; Marrs, C.F.

J. Bacteriol. 173, 4000-4006, 1991

A:Title: Interesting sequence differences between the pilin gene inversion regions of M.

A:Reference number: A42460; MUID:91286182

A:Accession: A42460

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-164 <ROZ>

A:Cross-references: GB:M59711

C:Genetics:

A:Genome: plasmid

C:Superfamily: gonococcal fimbrial protein

C:Keywords: methylated amino end

F:7/Modified site: methylated amino end (Phe) (in mature form) #status predicted

Query Match 31.8%; Score 204; DB 2; Length 164;

Best Local Similarity 35.3%; Pred. No. 2.5e-11;

Matches 48; Conservative 22; Mismatches 42; Indels 24; Gaps 5;

QY 8 ARTQVTRAVSEVSAALKTAESAILEGKEIYSSATPKDYOYDIGFTESTLLDGSQSIQ 63
 Db 35 SKSQTTRVVGELAAKTAAGTAVDALFEKPEVLDAGNTATSKEDIGLSTGGKA 86

QY 64 QIOVTDNKDGIV-----ELVATILGKSSGSAIKGAVITVSRKNDGVNCKITR-T 111
 Db 87 RSNLKEKGVVLAAGFASSTSSGTTGTLGNRANNDISGAIITQKRANDGVWTCVHOGCT 146

QY 112 PTAMKPNYAPANCPS 127
 Db 147 ATGWRDKRPIPTGCTNT 162

RESULT 4

A24434

beta fimbrial protein precursor - Moraxella bovis

N:Alternate names: beta pilin

C:Species: Moraxella bovis

C:Date: 08-Aug-1987 #sequence_revision 08-Aug-1987 #text_change 26-Aug-1999

C:Accession: A24434; JI0072

R:Marx, C.F.; Schoolnik, G.; Komey, J.M.; Hardy, J.; Rothbard, J.; Falkow, S.

J. Bacteriol. 163, 132-139, 1995

A:Reference number: A24434; MUID:85234350

A:Accession: A24434

A:Molecule type: DNA

A:Residues: 1-157 <MAR>

A:Cross-references: GB:M11435; NID:q149760; PIDN:AAA25304.1; PID:q149761

A:Experimental source: strain Epp63

R:Ruehl, W.W.; Marrs, C.F.; Fernandez, R.; Falkow, S.; Schoolnik, G.K.

J. Exp. Med. 168, 983-1002, 1988

A:Title: Purification, characterization, and pathogenicity of Moraxella bovis pilin.

A:Reference number: JI0071; MUID:89010522

A:Accession: JI0072

A:Molecule type: protein

A:Residues: 7-86, 93-122 <RUE>

A:Note: about 50% of the amino-terminus is N-methylated; the remaining 50% of the molec

C:Superfamily: gonococcal fimbrial protein

C:Keywords: methylated amino end; surface antigen

F:1-6/Domain: propeptide #status predicted <PRO>

F:7-157/Product: beta fimbrial protein 1 #status experimental <MAT>

F:8-157/Product: beta fimbrial protein 2 #status experimental <MA2>

F:7/Modified site: methylated amino end (Phe) (in mature form) #status experimental

F:136-155/Disulfide bonds: #status experimental

Query Match 29.4%; Score 189; DB 2; Length 157;

Best Local Similarity 36.9%; Pred. No. 5.4e-10;

Matches 48; Conservative 17; Mismatches 43; Indels 22; Gaps 5;

QY 8 ARTQVTRAVSEVSAALKTAESAILEGKEIYSSATPK-----DFOYDIGFTESTLLDGSQ 61
 Db 35 SKSQTTRVVGELAAKTAAGTAVDALFEK-----TPRLGNAANDIEDIGLITTTGGTA 85

QY 62 KQIOVTDN-----KDGVVELVATILGKSSGSAIKGAVITVSRKNDGVNCKITR-TPTA 114
 Db 86 RSNLMSVNVIGGAPATGAGTLEATLGNRANNDIGAVITQSDRDEGVWTCVINGSAAPG 145

QY 115 WKPNYAPANC 124
 Db 146 WKSKEVPTGC 155

RESULT 5

A41490

pilin precursor - Moraxella bovis

C:Species: Moraxella bovis

C:Date: 10-Apr-1992 #sequence_revision 10-Apr-1992 #text_change 26-Aug-1999

C:Accession: A41490

R:Ellerman, T.C.; Hoyle, P.A.; Lepper, A.W.D.

Infect. Immun. 58, 1678-1684, 1990

A:Title: Characterization of the pilin gene of Moraxella bovis Dalton 2d and express

A:Reference number: A41490; MUID:90256243

A:Accession: A41490

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-156 <ELL>

A:Cross-references: GB:992155; GB:M32665; NID:q149758; PIDN:AAA53087.1; PID:q149759

C:Superfamily: gonococcal fimbrial protein

C:Keywords: methylated amino end

F:7/Modified site: methylated amino end (Phe) (in mature form) #status predicted

Query Match 28.2%; Score 181; DB 2; Length 156;

Best Local Similarity 33.1%; Pred. No. 2.8e-09;

Matches 40; Conservative 26; Mismatches 49; Indels 6; Gaps 3;

QY 8 ARTQVTRAVSEVSAALKTAESAILEGKEIYSSATPKDYOYDIGFTESTLLDGSQSIQ 66
 Db 35 SKSQTTRVVGELAAKTAAGTAVDALFEKTPVNPSSADGIAVDIGLGEAATPRSNLSAVS 94

QY 67 VTDNR--DGTVELVATILGKSSGSAIKGAVITVSRKNDGVNCKITRTPAMKPNYAPAN 123
 Db 95 STFTKGSNGTIS--GTIGNNANDHIGTVISQERATGWSCVNGTGMWDKFIPTG 152

QY 124 C 124
 Db 153 C 153

RESULT 6

JI0071

alpha-pilin - Moraxella bovis (strain Epp63)

C:Species: Moraxella bovis

A:Note: host Bos primigenius taurus (cattle)

C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 08-Nov-1996

C:Accession: JI0071

R:Ruehl, W.W.; Marrs, C.F.; Fernandez, R.; Falkow, S.; Schoolnik, G.K.

J. Exp. Med. 168, 983-1002, 1988

A:Title: Purification, characterization, and pathogenicity of Moraxella bovis pilin.

A:Reference number: J10071; MUID:89010522

A:Accession: J10071

A:Molecule type: protein

A:Residues: 1-155 <RUE>

A:Note: about 50% of the amino-terminus is N-methylated; the remaining 50% of the molecule is N-methylated DNA sequence evidence indicated 117-Thr and 120-Thr, which were not C:Superfamily: gonococcal fimbrial protein

C:Keywords: methylated amino end

F:1-155/Product: alpha-pilin 1 #status experimental <MAT1>

F:2-155/Product: alpha-pilin 2 #status experimental <MAT2>

F:1/Modified site: methylated amino end (Phe) #status experimental

F:131-150/Disulfide bonds: #status experimental

Query Match

Best Local Similarity 26.1%; Score 167.5; DB 2; Length 155;
Matches 44; Conservative 21; Mismatches 50; Indels 9; Gaps 4;

OY 8 ARQVTRAVSEVSAALKTAESAILEGKEIVSATPKDYDIGFT---STLDDSGKSGQ 64

DB 29 SKQVTRVSEVSAALKTAESAILEGKEIVSATPKDYDIGFT---STLDDSGKSGQ 88

OY 65 IOVT---DNKDGTVELVATLGGSSGSAIKGAVITVSRKNDGVMNCKITKTPTA-WKPNYA 120

DB 89 VELTGFADNAGTIS--ATLGNKANKDIATVITIOERTTGGWTKIDGSOAAKYEKEN 146

OY 121 PANC 124

DB 147 PTGC 150

RESULT 7

A47699

type 4 pilin - Eikenella corrodens

N:Alternate names: N-methylphenylalanine-type pilin

C:Species: Eikenella corrodens

C>Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 26-Aug-1999

C:Accession: A47699; S23844

R:Rao, V.K.; Proguiske-Fox, A.

J. Gen. Microbiol. 139, 651-660, 1993

A:Title: Cloning and sequencing of two type 4 (N-methylphenylalanine) pilin genes from E

A:Reference number: A47699; MUID:93232782

A:Accession: A47699

A:Molecule type: DNA

A:Residues: 1-159 <RAO>

A:Cross-references: EMBL:212609; NID:941329; PIDN:CAA78250.1; PID:941330

A:Experimental source: ATCC 23834

A:Note: sequence extracted from NCBI backbone (NCBIRP:130001)

C:Genetics:

A:Gene: ecpA

C:Superfamily: gonococcal fimbrial protein

C:Keywords: methylated amino end

F:8/Modified site: methylated amino end (Phe) (in mature form) #status predicted

Query Match

Best Local Similarity 25.9%; Score 166; DB 2; Length 159;
Matches 42; Conservative 22; Mismatches 43; Indels 26; Gaps 4;

OY 8 ARQVTRAVSEVSAALKTAESAILEGKEIV---SSATPK-----DTGYDIGFT 52

DB 36 SKQVTRVSEVSAALKTAESAILEGKEIVPLAATAAGAAATPPENWGMIDNTSILS 95

OY 53 ESTLLDSSGKSGQIOVTDNKGTVELVATLGGSSGSAIKGAVITVSRKNDGVMNCKITKT 111

DB 96 AATLTGPGANA-----GDVTFVGTLTGEMANNSIHGATITLTCAASGEMTCAVAGT 145

OY 112 PTAMKPNYAPANC 124

DB 146 ATGKTKTKEVPSGC 158

RESULT 8

S15266
Fima protein - Dichelobacter nodosus

C:Species: Dichelobacter nodosus

C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 26-Aug-1999

C:Accession: S15266

R:Metlick, J.S.; Anderson, B.J.; Cox, P.T.; Dalrymple, B.P.; Bills, M.M.; Hobbs, M.;

Mol. Microbiol. 5, 561-573, 1991

A:Title: Gene sequences and comparison of the fimbrial subunits representative of Ba

A:Reference number: S15266; MUID:91260440

A:Accession: S15266

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-156 <MAT>

A:Cross-references: EMBL:X52389; NID:939696; PIDN:CAA36618.1; PID:939697

C:Superfamily: gonococcal fimbrial protein

C:Keywords: methylated amino end

F:8/Modified site: methylated amino end (Phe) (in mature form) #status predicted

Query Match

Best Local Similarity 25.0%; Score 160.5; DB 2; Length 156;
Matches 42; Conservative 24; Mismatches 36; Indels 31; Gaps 5;

OY 8 ARQVTRAVSEVSAALKTAESAILEGKEIVSATPKDYDIGFTSTLDDG----- 59

DB 36 ARQVTRVSEVSAALKTAESAILEGKEIVSATPKDYDIGFTSTLDDG----- 87

OY 60 ---SGKSGQI---QVTDNKGTVELVATLGGSSGSAIKGAVITVSRKNDGVMNCKITKT 111

DB 88 TAAATGCGAGITIKKPVVADDEGNT--VATFGRNAAALIKPQTLTMSRSKEGTWC----- 140

OY 112 PTAMKPNYAPANC 124

DB 141 ATTVEAKFQPTGC 153

RESULT 9

A46566

pilin precursor - Dichelobacter nodosus (strain 340, serogroup D)

C:Species: Dichelobacter nodosus

C>Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 26-Aug-1999

C:Accession: A46566

R:Finney, K.G.; Eilman, T.C.; Stewart, D.J.

J. Gen. Microbiol. 134, 575-584, 1988

A:Title: Nucleotide sequence of the pilin gene of Bacteroides nodosus 340 (serogroup

A:Reference number: A46566; MUID:89036113

A:Accession: A46566

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-157 <FIN>

A:Cross-references: GB:M20369; NID:9145064; PIDN:AAA23347.1; PID:9145065

C:Superfamily: gonococcal fimbrial protein

C:Keywords: methylated amino end

F:8/Modified site: methylated amino end (Phe) (in mature form) #status predicted

Query Match

Best Local Similarity 25.0%; Score 160.5; DB 2; Length 157;
Matches 42; Conservative 24; Mismatches 36; Indels 31; Gaps 5;

OY 8 ARQVTRAVSEVSAALKTAESAILEGKEIVSATPKDYDIGFTSTLDDG----- 59

DB 36 ARQVTRVSEVSAALKTAESAILEGKEIVSATPKDYDIGFTSTLDDG----- 87

OY 60 ---SGKSGQI---QVTDNKGTVELVATLGGSSGSAIKGAVITVSRKNDGVMNCKITKT 111

DB 88 TAAATGCGAGITIKKPVVADDEGNT--VATFGRNAAALIKPQTLTMSRSKEGTWC----- 140

OY 112 PTAMKPNYAPANC 124

DB 141 ATTVEAKFQPTGC 153

RESULT 10

A55851
 prepilin - Moraxella bovis
 C:Species: Moraxella bovis
 C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 26-Aug-1999
 C:Accession: A55851
 R:Atwell, J.L.; Jemmett, J.M.; Lepper, A.W.; Ellemann, T.C.
 J. Bacteriol. 176, 4875-4882, 1994
 A:Title: Characterization of pilin genes from seven serologically defined prototype strains
 A:Reference number: A55851; MUID:94327452
 A:Accession: A55851
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-158 <RES>
 A:Cross-references: GB:L32965; NID:9488303; PIDN:AAA5558.1; PID:9488304
 C:Superfamily: gonococcal fimbrial protein
 C:Keywords: methylated amino end
 F:7/Modified site: methylated amino end (Phe) (in mature form) #status predicted

Query Match 23.5%; Score 151; DB 2; Length 158;
 Best Local Similarity 31.5%; Pred. No. 1.4e-06;
 Matches 39; Conservative 21; Mismatches 54; Indels 10; Gaps 3;

OY 8 ARTQVRAVSEVSAIKTAESAILEGKEIVSSATPKDYOYDIGFTSTLLDGSQSQIOY 67
 DB 35 SKQOTRVRVGEIAAGKTADVALEEGKTPVIGTTTITTEDIGLTTA---GGTPRSNLVS 91
 OY 68 TDNKKD-----GTVELVATLGKSSGSAIKGAVTVSRKNDGVNCKITKT-PTAMKPNTA 120
 DB 92 AVTLDDGAFATGEGSTKAVLGTANNDIAGAEIKOIRNDGQVSCVKAAGAFGFKDPI 151
 OY 121 PANC 124
 DB 152 PTGC 155

RESULT 11

A37167
 pilin precursor - Dichelobacter nodosus (strain 351)
 C:Species: Dichelobacter nodosus
 C>Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 26-Aug-1999
 C:Accession: A37167
 R:Hoyle, P.A.; Ellemann, T.C.; McKern, N.M.; Stewart, D.J.
 J. Gen. Microbiol. 135, 1113-1122, 1989
 A:Title: Sequence of pilin from Bacteroides nodosus 351 (serogroup H) and implications for
 A:Reference number: A37167; MUID:9015189
 A:Accession: A37167
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-160 <HOY>
 A:Cross-references: GB:M26980; NID:9145042; PIDN:AAA23336.1; PID:9145043
 C:Superfamily: gonococcal fimbrial protein
 C:Keywords: methylated amino end
 F:8/Modified site: methylated amino end (Phe) (in mature form) #status predicted

Query Match 20.8%; Score 133.5; DB 2; Length 160;
 Best Local Similarity 27.8%; Pred. No. 5.3e-05;
 Matches 37; Conservative 22; Mismatches 45; Indels 29; Gaps 4;

OY 8 ARTQVRAVSEVSAIKTAESAILEGKEIVSSATPKDYOYDIGFTSTLLDGSQSQIO- 66
 DB 36 ARSOVSRVSEFGOMRTAIECTLDGK-----KADECFIGWTSNLLGASGSPSSSN 87
 OY 67 -----VTDNK-----DGVELVATLGKSSGSAIKGAVTVSRKNDGVNCKITKT 111
 DB 88 DSTADHGGGGLVYDKLEADATNATTAATPGONAAATLHGKALKWTRDPKATWSCS---- 143
 OY 112 PTAMKPNTA 124
 DB 144 -TDVELKFRPTGC 155

RESULT 12

B47699
 N-methylphenylalanine pilin type 4 - Elkenella corrodens
 C:Species: Elkenella corrodens
 C>Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
 C:Accession: B47699; S23845
 R:Rao, V.K.; Prognulski-Fox, A.
 J. Gen. Microbiol. 139, 651-660, 1993
 A:Title: Cloning and sequencing of two type 4 (N-methylphenylalanine) pilin genes
 A:Reference number: A47699; MUID:93232782
 A:Accession: B47699
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-159 <RAO>
 A:Cross-references: EMBL:212609; NID:941329; PIDN:CAA78251.1; PID:941331
 A:Experimental source: ATCC 23834
 A:Note: sequence extracted from NCBI backbone (NCBIN:130000, NCBIPI:130002)
 C:Superfamily: gonococcal fimbrial protein

Query Match 20.6%; Score 132.5; DB 2; Length 159;
 Best Local Similarity 30.7%; Pred. No. 6.5e-05;
 Matches 39; Conservative 17; Mismatches 56; Indels 15; Gaps 3;

OY 8 ARTQVRAVSEVSAIKTAESAILEGKEIVSSATPKDYOYDIGFTSTLLDGSQSQ--- 64
 DB 35 AKAQINRVEYELGSTRKAVESILANG-----GIPVDSOGGVONSRRLEFLGINQPN 89
 OY 65 -----IOYTDNKKDQTVELVATLGKSSGSAIKGAVTVSRKNDGVNCKITKTPTAW-KP 117
 DB 90 SNLITFASVGLNSOFERNVATFGRNALPOIGAVISFVRDNGQVCEIDKSNAAVCP 149
 OY 118 NYAPANC 124
 DB 150 KYTPATC 156

RESULT 13

S15267
 fima protein - Dichelobacter nodosus
 C:Species: Dichelobacter nodosus
 C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 26-Aug-1999
 C:Accession: S15267
 R:Metlick, J.S.; Anderson, B.J.; Cox, P.T.; Dalrymple, B.P.; Bills, M.M.; Hobbs, M.;
 Mol. Microbiol. 5, 561-573, 1991
 A:Title: Gene sequences and comparison of the fimbrial subunits representative of Ba.
 A:Reference number: S15267; MUID:91260440
 A:Accession: S15267
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-156 <MAT>
 A:Cross-references: EMBL:X52390; NID:939703; PIDN:CAA36619.1; PID:939704
 C:Superfamily: gonococcal fimbrial protein
 C:Keywords: methylated amino end
 F:8/Modified site: methylated amino end (Phe) (in mature form) #status predicted

Query Match 20.6%; Score 132; DB 2; Length 156;
 Best Local Similarity 30.4%; Pred. No. 7e-05;
 Matches 38; Conservative 23; Mismatches 40; Indels 24; Gaps 5;

OY 8 ARTQVRAVSEVSAIKTAESAILEGKEIVSSATPKDYOYDIGFTSTLLDGSQSQ--- 64
 DB 36 ARSOVSRVSEFGOMRTAIECTLDGKE-----GKDC--FIGWTSNLLAAGSSTNN 87
 OY 65 -----IOYTDNKKDQTVELVATLGKSSGSAIKGAVTVSRKNDGVNCKITKTPT 112
 DB 88 ATAEDPGGGLNTITVALGSAENKTEATFGONAAATLHGKALKWTRSPKATWSCS--TVD 146
 OY 113 TAMKP 117
 DB 147 EKFKP 151

RESULT 14

S52692
fimbriillin - Xanthomonas campestris
C:Species: Xanthomonas campestris
C>Date: 19-May-1995 #sequence_revision 01-Sep-1995 #text_change 24-Nov-1999
C/Accession: S52692
R:Ojaneen, T.M.; Kalkkinen, N.; Westerlund, B.; van Doorn, J.; Haahela, K.; Korhonen, T.
submitted to the EMBL Data Library, March 1995
A:Description: Characterization of the fimA gene encoding the type IV fimbriillin of the
A:Reference number: S52692
A:Accession: S52692
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-136 <OJA>
A:Cross-references: EMBL:Z48759; NID:G747907; PIDN:CAA8680.1; PID:G747908
C:Superfamily: gonococcal fimbrial protein

Query Match

20.1%; Score 129; DB 2; Length 136;
Best Local Similarity 30.8%; Pred. No. 0.00011;

Matches 37; Conservative 16; Mismatches 49; Indels 18; Gaps 3;

OY 8 ARTQVTRAVSEVSAKTAESAII--LEGEIV--SSATPKDQYDIGFTSTLDSGSKSIQV 67

DB 35 AKSQVTAGLAELNPGKTYEVALNEGKTYVAD-----ITELGLKSPSERCTIAP 83

OY 68 TDNKDGTVELVATLKGSSGSAIKGAVTVSRKNDGVNCKITKPTAMKPNVAPANCPNS 127

DB 84 ITALSATGTIECTL--KGNTOVGKVTLTRANDGTWTCR-----TDALKKYPAGCGCA 136

RESULT 15

A43504

pilin precursor - Pseudomonas aeruginosa

C:Species: Pseudomonas aeruginosa

C>Date: 21-Oct-1992 #sequence_revision 21-Oct-1992 #text_change 29-Jan-1999

C/Accession: A43504

R:Pasloske, B.L.; Joffe, A.M.; Sun, Q.; Volpel, K.; Paranchych, W.; Eftekhari, F.; Speerth

Infect. Immun. 56, 665-672, 1988

A:Title: Serial isolates of Pseudomonas aeruginosa from a cystic fibrosis patient have

A:Reference number: A43504; MID:86138467

A:Accession: A43504

A>Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-150 <PAS>

A:Cross-references: GB:M24281

C:Superfamily: gonococcal fimbrial protein

C:Keywords: methylated amino end

F:7/Modified site: methylated amino end (Phe) (in mature form) #status predicted

Query Match

18.8%; Score 121; DB 2; Length 150;
Best Local Similarity 28.7%; Pred. No. 0.00065;

Matches 35; Conservative 26; Mismatches 47; Indels 14; Gaps 6;

OY 8 ARTQVTRAVSEVSAKTAESAII--LEGEIV--SSATPKDQYDIGFTSTLDSGSK 62

DB 35 ARSEGASALATINPLKTTVESLSRGLAGSKILIGTASTADITY--VGIDEKA--NKLGT 91

OY 63 SQIOVTDNKGTVELVATLKGSSGSAIKGAVTVSRKNDGVNCKITKPTAMKPNVAPA 122

DB 92 VAVTIKIDTGDVTFEATGOSSPKN--AGKEITLRTAEGVWCTCTSTO-----EEMFIPK 145

OY 123 NC 124

DB 146 GC 147

Fri Feb 8 15:44:56 2002

us-09-865-159-8.rpt

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 8, 2002, 15:34:22 ; Search time 22.14 Seconds
(without alignments)
210.318 Million cell updates/sec

Title: US-09-865-159-8

Perfect score: 642
Sequence: 1 ALEGEFFARTQVTRAVSEVS.....ITKPTANKPNTPANCENS 127

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues
Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	601	93.6	154	1	FMK1_PSEAE
2	597	93.0	154	1	FMK1_PSEAE
3	189	29.4	157	1	FMK1_PSEAE
4	167.5	26.1	159	1	FMK1_PSEAE
5	166	25.9	159	1	FMK1_PSEAE
6	160.5	25.0	156	1	FMK1_PSEAE
7	135	21.0	156	1	FMK1_PSEAE
8	133.5	20.8	160	1	FMK1_PSEAE
9	132.5	20.6	159	1	FMK1_PSEAE
10	121	18.8	150	1	FMK1_PSEAE
11	117	18.2	150	1	FMK1_PSEAE
12	112	17.4	149	1	FMK1_PSEAE
13	99	15.4	150	1	FMK1_PSEAE
14	98	15.3	159	1	FMK1_PSEAE
15	96	15.0	136	1	FMK1_PSEAE
16	95	14.8	159	1	FMK1_PSEAE
17	84	13.1	263	1	FMK1_PSEAE
18	82.5	12.9	240	1	FMK1_PSEAE
19	81	12.6	516	1	FMK1_PSEAE
20	79.5	12.4	273	1	FMK1_PSEAE
21	79	12.3	934	1	FMK1_PSEAE
22	77	12.0	493	1	FMK1_PSEAE
23	76.5	11.9	162	1	FMK1_PSEAE
24	76.5	11.9	241	1	FMK1_PSEAE
25	76.5	11.9	348	1	FMK1_PSEAE
26	76.5	11.9	358	1	FMK1_PSEAE
27	76	11.8	152	1	FMK1_PSEAE
28	75.5	11.8	551	1	FMK1_PSEAE
29	75	11.7	258	1	FMK1_PSEAE
30	75	11.7	600	1	FMK1_PSEAE
31	74.5	11.6	518	1	FMK1_PSEAE
32	74	11.5	1242	1	FMK1_PSEAE
33	72	11.2	502	1	FMK1_PSEAE

ALIGNMENTS

RESULT	ID	FMK1_PSEAE	STANDARD	PRT	154 AA
34	71.5	11.1	513	1	YJIV_ECOLI
35	71.5	11.1	599	1	HS75_SPTOL
36	71.5	11.1	706	1	HS75_PEA
37	71.5	11.1	792	1	CADB_CHICK
38	71.5	11.1	1938	1	MYH2_HUMAN
39	71	11.1	1748	1	POLR_ELV
40	70.5	11.0	216	1	RS5_METV
41	70.5	11.0	496	1	GLPK_BACSU
42	70.5	11.0	661	1	HS7C_CAEEL
43	70	10.9	274	1	OSAA_BORBU
44	70	10.9	347	1	VCAA_BPT3
45	70	10.9	433	1	ELT2_CAEEL

RESULT 1
FMK1_PSEAE
ID FMK1_PSEAE STANDARD PRT 154 AA.

AC P17836;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE FILTRIAL PROTEIN PRECURSOR (PILIN) (STRAIN K122-4).
GN PILA OR FILA.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OX Pseudomonas.
NCBI_Taxid=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K122-4;
RA MEDLINE=88298689; PubMed=2841299;
RX Pasloske B.L., Sastri P.A., Finlay B.B., Paranchych W.;
RT "Two unusual pilin sequences from different isolates of Pseudomonas aeruginosa."
RL J. Bacteriol. 170:3738-3741(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-9D2;
RA MEDLINE=94131566; PubMed=7507890;
RX Castic P.A., Deal C.D.;
RT "Differentiation of Pseudomonas aeruginosa pilin based on sequence and B-cell epitope analyses."
RL Infect. Immun. 62:371-376(1994).
CC -1- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4 NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.
CC -1- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M21652; AAC63060.1; -
CC EMBL: S68100; AAC60460.1; -
CC PIR: B31105; B31105.
CC HSSP: P02974; IAY2.
CC InterPro: IPR001082; Prok_N_methyltn.
CC Pfam: PF00114; Pilin; 1.
CC ProDom: PD000666; Pilin; 1.
CC PROSITE: PS00409; PROKAR_NTER_METHYL. 1.
CC Fimbrin; Methylation.
CC FIMBRIAL PROTEIN.
CC METHYLATION (BY SIMILARITY).
FT MOD_RES 7 154
FT CHAIN 7 7
FT

FT DISULFID 133 151 BY SIMILARITY.
SQ SEQUENCE 154 AA; 16278 MW; 807409FABCC6AD0 CRC64;

Query Match
Best Local Similarity 93.6%; Score 601; DB 1; Length 154;
Matches 119; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 ARTQVTRAVSEVSAIKTAESAILEGKEIVSSATPKDTQYDIGFTSTLLDGSQIOY 67
DB 35 ARTQVTRAVSEVSAIKTAESAILEGKEIVSSATPKDTQYDIGFTSTLLDGSQIOY 94
QY 68 TDNKGVEIVATLTKSSGSAIKGAVITVSRKNDGVWNNCKITKPTAMKPNYAPANCPS 127
DB 95 TDNKGVEIVATLTKSSGSAIKGAVITVSRKNDGVWNNCKITKPTAMKPNYAPANCPS 154

RESULT 2
FM12_PSEAE STANDARD; PRT; 154 AA.
ID FM12_PSEAE
AC P18774;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE FIMBRIAL PROTEIN PRECURSOR (PILIN) (STRAIN 1244).
GN PILA OR FILA.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
ON NCBI_Taxid=287;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=69281493; PubMed=2499765;
RA Castle P.A., Siderly H.F., Sadoff J.C.;
RT "Cloning and sequencing of the Pseudomonas aeruginosa 1244 pilin structural gene."
RL Mol. Gen. Genet. 216:75-80(1989).
CC -1- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4 NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.
CC -1- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X83916; CAA58768.1; -
DR PIR: S04440; S04440.
DR HSSP: P02974; 1AY2.
DR InterPro: IPR001082; Pilin.
DR InterPro: IPR001120; Prok_N_methyltn.
DR Pfam: PF00114; Pilin; 1.
DR ProDom: PD000666; Pilin; 1.
DR PROSITE: PS00409; PROKR_NTER_METHYL; 1.
KW Fimbria; Methylation.
FT PROPEP 1 6
FT CHAIN 7 154 FIMBRIAL PROTEIN.
FT MOD_RES 7 7 METHYLATION (BY SIMILARITY).
FT DISULFID 133 151 BY SIMILARITY.
SQ SEQUENCE 154 AA; 16277 MW; 9A6E9E0A6C66AD0 CRC64;

Query Match
Best Local Similarity 93.0%; Score 597; DB 1; Length 154;
Matches 118; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 ARTQVTRAVSEVSAIKTAESAILEGKEIVSSATPKDTQYDIGFTSTLLDGSQIOY 67
|||||
|||||

DB 35 ARTQVTRAVSEVSAIKTAESAILEGKEIVSSATPKDTQYDIGFTSTLLDGSQIOY 94
QY 68 TDNKGVEIVATLTKSSGSAIKGAVITVSRKNDGVWNNCKITKPTAMKPNYAPANCPS 127
DB 95 TDNKGVEIVATLTKSSGSAIKGAVITVSRKNDGVWNNCKITKPTAMKPNYAPANCPS 154
RESULT 3
FMO_MORBO STANDARD; PRT; 157 AA.
ID FMO_MORBO
AC P07640;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE FIMBRIAL PROTEIN Q PRECURSOR (BETA PILIN) (Q PILIN).
GN TFPO.
OS Moraxella bovis.
OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae; Moraxella.
ON NCBI_Taxid=476;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Epp63;
RC MEDLINE=85234350; PubMed=2861194;
RA Marrs C.F., Schoolnik G., Komey J.M., Hardy J., Rothbard J., Falkow S.;
RT "Cloning and sequencing of a Moraxella bovis pilin gene."
RL J. Bacteriol. 163:132-139(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=Epp63;
RC MEDLINE=90094235; PubMed=2403542;
RA Fuls K.A., Marrs C.F., Stevens S.P., Green M.R.;
RT "Sequence analysis of the inversion region containing the pilin genes of Moraxella bovis."
RL J. Bacteriol. 172:310-316(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=9126182; PubMed=2061282;
RA Rozsa F.W., Marrs C.F.;
RT "Interesting sequence differences between the pilin gene inversion regions of Moraxella lacunata ATCC 17956 and Moraxella bovis Epp63."
RL J. Bacteriol. 173:4000-4006(1991).
RN [4]
RP SEQUENCE OF 7-157.
RX MEDLINE=89010522; PubMed=2902184;
RA Ruehl W.W., Marrs C.F., Fernandez R., Falkow S., Schoolnik G.K.;
RT "Purification, characterization, and pathogenicity of Moraxella bovis pilin."
RL J. Exp. Med. 168:983-1002(1988).
CC -1- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4 NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.
CC -1- MISCELLANEOUS: MORAXELLA BOVIS CAN EXPRESS EITHER A Q OR A I PILIN, THE INVERSION OF 2 KB OF DNA DETERMINES WHICH PILIN IS EXPRESSED.
CC -1- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M1435; AAA25304.1; -
DR EMBL: M32345; AAA88223.1; -
DR EMBL: M59712; AAA25308.1; -
DR PIR: A24434; A24434.
DR PIR: J10072; J10072.
DR InterPro: IPR001082; Pilin.
DR InterPro: IPR001120; Prok_N_methyltn.

DR Pfam; PF00114; pilin; 1.
 DR ProDom; PD000666; pilin; 1.
 DR PROSITE; PS00409; PROKAR_NTER_METHYL; 1.
 KW Fimbria; Methylation.
 FT PROPEP 1 6
 FT CHAIN 7 157 FIMBRIAL PROTEIN Q.
 FT MOD_RES 7 7 METHYLATION.
 FT DISULFID 136 155 BY SIMILARITY.
 SQ SEQUENCE 157 AA; 16006 MW; A923CD8A26C693C9 CRC64;

Query Match 29.4%; Score 189; DB 1; Length 157;
 Best Local Similarity 36.9%; Pred. No. 2.3e-09;
 Matches 48; Conservative 17; Mismatches 43; Indels 22; Gaps 5;

OY 8 ARTQVTRAVSEVSLKTAESAILEGKEIVSSAPPK-----DPOYDIGFESTLDDSG 61
 Db 35 SKSQTRVVGELAGKTAVDALFEGR-----TPKLGKANDTEEDIGLTTT---GGTA 85
 OY 62 KSOIQVTDN-----KQGTVELVATLCKSSGSAIKGAVITVSRKNDGVWNCKIT-KTPPTA 114
 Db 86 RSNLMSSVNIIGGAFATGATGTLGNRANKDIAGAVITQSRDAEGVWCTCTINGSAAPG 145
 OY 115 WKPNTAPANC 124
 Db 146 WKSKEVPTGC 155

RESULT 4

FIM_MORBO
 ID FIM_MORBO STANDARD; PRT; 159 AA.

AC P20657;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE FIMBRIAL PROTEIN I PRECURSOR (ALPHA PILIN) (I PILIN).
 OS Moraxella boyis.
 OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae; Moraxella.
 OX NCBI_TaxID=476;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-EPP63;
 RX MEDLINE=90094235; PubMed=2403542;
 RA Fulk K.A., Marrs C.F., Stevens S.P., Green M.R.;
 RT "Sequence analysis of the inversion region containing the pilin genes
 of Moraxella boyis.";
 RT J. Bacteriol. 172:310-316(1990).
 RN [2]
 RP SEQUENCE OF 7-159.
 RX MEDLINE=89010522; PubMed=2902184;
 RA Ruchl W.W., Marrs C.F., Fernandez R., Falkow S., Schoolnik G.K.;
 RT "Purification, characterization, and pathogenicity of Moraxella boyis
 pilin.";
 RT J. Exp. Med. 168:983-1002(1988).
 CC -1- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
 NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
 CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
 CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED FILUS.
 CC -1- MISCELLANEOUS: MORAXELLA BOVIS CAN EXPRESS EITHER A Q OR A I
 PILIN. THE INVERSION OF 2 KB OF DNA DETERMINES WHICH PILIN IS
 EXPRESSED.
 CC -1- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC
 CC EMBL; M32345; -; NOT_ANNOTATED_CDS.
 DR PIR; J10071; J10071.

DR HSSP; P02974; IAY2.
 DR InterPro; IPR001082; pilin.
 DR InterPro; IPR001120; Prok_N_methyltn.
 DR Pfam; PF00114; pilin; 1.
 DR ProDom; PD000666; pilin; 1.
 KW Fimbria; Methylation.
 FT PROPEP 1 6
 FT CHAIN 7 159 FIMBRIAL PROTEIN I.
 FT MOD_RES 7 7 METHYLATION.
 FT CONFLICT 159 159 K -> KSK (IN REF. 2).
 SQ SEQUENCE 159 AA; 16723 MW; 9130E2285C7E679E CRC64;

Query Match 26.1%; Score 167.5; DB 1; Length 159;
 Best Local Similarity 35.5%; Pred. No. 1.5e-07;
 Matches 44; Conservative 21; Mismatches 50; Indels 9; Gaps 4;

OY 8 ARTQVTRAVSEVSLKTAESAILEGKEIVSSAPPKDYDIGFTE---STLLDGSQSQ 64
 Db 35 SKSQTRVVGELAGKTAVDALFEGRTPVSEESTSKENIGLTSSTSTPRSNLMAS 94
 OY 65 IOVT---DNKGTVELVATLCKSSGSAIKGAVITVSRKNDGVWNCKITKTPPTA-WKPNTA 120
 Db 95 VELTGFADNGAGTIS--ATLGKANKDKIAKTYITERTTDGVTCKIDGSOAKIKKFN 152
 OY 121 PANC 124
 Db 153 PTGC 156

RESULT 5

ECPA_EIKCO
 ID ECPA_EIKCO STANDARD; PRT; 159 AA.

AC P35645;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE FIMBRIAL PROTEIN ECPA PRECURSOR (PILIN).
 DE ECPA.
 OS Eikenella corrodens.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Eikenella.
 OX NCBI_TaxID=539;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 23834;
 RX MEDLINE=93232782; PubMed=8473871;
 RA Rao V.K., Prognulski-Fox A.;
 RT "Cloning and sequencing of two type 4 (N-methylphenylalanine) pilin
 genes from Eikenella corrodens.";
 RT J. Gen. Microbiol. 139:651-660(1993).
 CC -1- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC
 CC EMBL; Z12609; CA878250.1; -
 DR PIR; S23844; S23844.
 DR PIR; A47699; A47699.
 DR HSSP; P02974; IAY2.
 DR InterPro; IPR001082; pilin.
 DR InterPro; IPR001120; Prok_N_methyltn.
 DR Pfam; PF00114; pilin; 1.
 DR ProDom; PD000666; pilin; 1.
 DR PROSITE; PS00409; PROKAR_NTER_METHYL; 1.
 KW Fimbria; Methylation.
 FT PROPEP 1 7
 FT CHAIN 8 159 POTENTIAL FIMBRIAL PROTEIN ECPA.

FT MOD_RES 8 8 METHYLATION (BY SIMILARITY).
 FT DISULFID 139 158 BY SIMILARITY.
 SQ SEQUENCE 159 AA; 16177 MW; 7C3DAD9A9B1BC2 CRC64;

Query Match 25.0%; Score 166; DB 1; Length 159;
 Best Local Similarity 31.6%; Pred. No. 2e-07;
 Matches 42; Conservative 22; Mismatches 43; Indels 26; Gaps 4;

OY 8 ARQVTRAVSEVSAIKTAESAILEGKEIV-----SSATPK-----DQYDIGFT 52
 DB 36 SKSVYTAAYGEMGTAKTAIFEGKTPVLAATAAGAAATPENEVGMIDNPTSNLLS 95
 OY 53 ESTLLDSSGKSQIQVTDNKGDTVELVATLGKSSGSAIKGAVITYSRKNDGVMNCKITKT 111
 DB 96 AATLTGPGANA-----GDVTFVGTLEGNANSSIHGATITLTCTAASEMTCAVAAGT 145
 OY 112 PTAMKPNYAPANC 124
 DB 146 ATGWKTKFPPSGC 158

RESULT 6

FMAD_BACNO STANDARD: PRT: 156 AA.

AC P13253; 01-JAN-1990 (Rel. 13, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE FIMBRIAL PROTEIN PRECURSOR (PILIN) (SEROGROUP D) (340 ANTIGEN).
 GN FIMA.

OS Bacteroides nodosus (Dichelobacter nodosus).
 OC Bacteria; Proteobacteria; gamma subdivision; Cardiobacteriaceae;
 OC Dichelobacter.

OX NCBI_TaxID=870;

RESULT 7

FMAD_BACNO STANDARD: PRT: 156 AA.

AC P13253; 01-JAN-1990 (Rel. 13, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE FIMBRIAL PROTEIN PRECURSOR (PILIN) (SEROGROUP D) (340 ANTIGEN).
 GN FIMA.

OS Bacteroides nodosus (Dichelobacter nodosus).
 OC Bacteria; Proteobacteria; gamma subdivision; Cardiobacteriaceae;
 OC Dichelobacter.

OX NCBI_TaxID=870;

AC P13253; 01-JAN-1990 (Rel. 13, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE FIMBRIAL PROTEIN PRECURSOR (PILIN) (SEROGROUP D) (340 ANTIGEN).
 GN FIMA.

OS Bacteroides nodosus (Dichelobacter nodosus).
 OC Bacteria; Proteobacteria; gamma subdivision; Cardiobacteriaceae;
 OC Dichelobacter.

OX NCBI_TaxID=870;

AC P13253; 01-JAN-1990 (Rel. 13, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE FIMBRIAL PROTEIN PRECURSOR (PILIN) (SEROGROUP D) (340 ANTIGEN).
 GN FIMA.

OS Bacteroides nodosus (Dichelobacter nodosus).
 OC Bacteria; Proteobacteria; gamma subdivision; Cardiobacteriaceae;
 OC Dichelobacter.

OX NCBI_TaxID=870;

AC P13253; 01-JAN-1990 (Rel. 13, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE FIMBRIAL PROTEIN PRECURSOR (PILIN) (SEROGROUP D) (340 ANTIGEN).
 GN FIMA.

OS Bacteroides nodosus (Dichelobacter nodosus).
 OC Bacteria; Proteobacteria; gamma subdivision; Cardiobacteriaceae;
 OC Dichelobacter.

OX NCBI_TaxID=870;

AC P13253; 01-JAN-1990 (Rel. 13, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE FIMBRIAL PROTEIN PRECURSOR (PILIN) (SEROGROUP D) (340 ANTIGEN).
 GN FIMA.

OS Bacteroides nodosus (Dichelobacter nodosus).
 OC Bacteria; Proteobacteria; gamma subdivision; Cardiobacteriaceae;
 OC Dichelobacter.

OX NCBI_TaxID=870;

AC P13253; 01-JAN-1990 (Rel. 13, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE FIMBRIAL PROTEIN PRECURSOR (PILIN) (SEROGROUP D) (340 ANTIGEN).
 GN FIMA.

OS Bacteroides nodosus (Dichelobacter nodosus).
 OC Bacteria; Proteobacteria; gamma subdivision; Cardiobacteriaceae;
 OC Dichelobacter.

OX NCBI_TaxID=870;

AC P13253; 01-JAN-1990 (Rel. 13, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE FIMBRIAL PROTEIN PRECURSOR (PILIN) (SEROGROUP D) (340 ANTIGEN).
 GN FIMA.

OS Bacteroides nodosus (Dichelobacter nodosus).
 OC Bacteria; Proteobacteria; gamma subdivision; Cardiobacteriaceae;
 OC Dichelobacter.

OX NCBI_TaxID=870;

AC P13253; 01-JAN-1990 (Rel. 13, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE FIMBRIAL PROTEIN PRECURSOR (PILIN) (SEROGROUP D) (340 ANTIGEN).
 GN FIMA.

OS Bacteroides nodosus (Dichelobacter nodosus).
 OC Bacteria; Proteobacteria; gamma subdivision; Cardiobacteriaceae;
 OC Dichelobacter.

DR InterPro: IPR001120; Prok_N_methylin.
 DR Pfam: PF00114; pilin; 1.
 DR ProDom: PD000666; pilin; 1.
 DR ProSITE: PS00409; PROKAR_NTER_METHYL; 1.
 KW Fimbrin; Methylation; 1.

FT CHAIN 1 156 FIMBRIAL PROTEIN.
 FT MOD_RES 8 8 METHYLATION (BY SIMILARITY).
 FT DISULFID 57 67 BY SIMILARITY.
 FT DISULFID 140 153 BY SIMILARITY.
 FT VARIANT 65 66 GE -> DK (IN ISOLATE 340).
 FT VARIANT 80 80 D -> E (IN ISOLATE 340).
 FT VARIANT 95 95 A -> T (IN ISOLATE 340).
 SQ SEQUENCE 156 AA; 16544 MW; 4541BCBC22BBE93C CRC64;

Query Match 25.0%; Score 160.5; DB 1; Length 156;
 Best Local Similarity 31.6%; Pred. No. 5.5e-07;
 Matches 42; Conservative 24; Mismatches 36; Indels 31; Gaps 5;

OY 8 ARQVTRAVSEVSAIKTAESAILEGKEIVSSATPRDQYDIGFTSTLLD----- 59
 DB 36 ARSQSVKSEVSEIGMRTALETCVLDGKEA-----GECFLGWTGNSNLDGPTAGTES 87
 OY 60 -----SGKSOI-----QYTDKDGTVELVATLGKSSGSAIKGAVITYSRKNDGVMNCKITKT 111
 DB 88 TAAATGQAGITTKYPAADDEGNI--VAATGNNAAAIKPPQTLWSRSKEGTWTC----- 140
 OY 112 PTAMKPNYAPANC 124
 DB 141 ATTVEAKFQPTGC 153

RESULT 7

FMAD_BACNO STANDARD: PRT: 156 AA.

AC P04953; 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 01-NOV-1991 (Rel. 20, Last annotation update)
 DE FIMBRIAL PROTEIN PRECURSOR (PILIN) (SEROGROUP H1) (265 ANTIGEN) (TWO SUBUNITS PILIN).
 GN FIMA.

OS Bacteroides nodosus (Dichelobacter nodosus).
 OC Bacteria; Proteobacteria; gamma subdivision; Cardiobacteriaceae;
 OC Dichelobacter.

OX NCBI_TaxID=870;

AC P04953; 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 01-NOV-1991 (Rel. 20, Last annotation update)
 DE FIMBRIAL PROTEIN PRECURSOR (PILIN) (SEROGROUP H1) (265 ANTIGEN) (TWO SUBUNITS PILIN).
 GN FIMA.

OS Bacteroides nodosus (Dichelobacter nodosus).
 OC Bacteria; Proteobacteria; gamma subdivision; Cardiobacteriaceae;
 OC Dichelobacter.

OX NCBI_TaxID=870;

AC P04953; 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 01-NOV-1991 (Rel. 20, Last annotation update)
 DE FIMBRIAL PROTEIN PRECURSOR (PILIN) (SEROGROUP H1) (265 ANTIGEN) (TWO SUBUNITS PILIN).
 GN FIMA.

OS Bacteroides nodosus (Dichelobacter nodosus).
 OC Bacteria; Proteobacteria; gamma subdivision; Cardiobacteriaceae;
 OC Dichelobacter.

OX NCBI_TaxID=870;

AC P04953; 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 01-NOV-1991 (Rel. 20, Last annotation update)
 DE FIMBRIAL PROTEIN PRECURSOR (PILIN) (SEROGROUP H1) (265 ANTIGEN) (TWO SUBUNITS PILIN).
 GN FIMA.

OS Bacteroides nodosus (Dichelobacter nodosus).
 OC Bacteria; Proteobacteria; gamma subdivision; Cardiobacteriaceae;
 OC Dichelobacter.

OX NCBI_TaxID=870;

AC P04953; 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 01-NOV-1991 (Rel. 20, Last annotation update)
 DE FIMBRIAL PROTEIN PRECURSOR (PILIN) (SEROGROUP H1) (265 ANTIGEN) (TWO SUBUNITS PILIN).
 GN FIMA.

OS Bacteroides nodosus (Dichelobacter nodosus).
 OC Bacteria; Proteobacteria; gamma subdivision; Cardiobacteriaceae;
 OC Dichelobacter.

OX NCBI_TaxID=870;

AC P04953; 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 01-NOV-1991 (Rel. 20, Last annotation update)
 DE FIMBRIAL PROTEIN PRECURSOR (PILIN) (SEROGROUP H1) (265 ANTIGEN) (TWO SUBUNITS PILIN).
 GN FIMA.

OS Bacteroides nodosus (Dichelobacter nodosus).
 OC Bacteria; Proteobacteria; gamma subdivision; Cardiobacteriaceae;
 OC Dichelobacter.

OX NCBI_TaxID=870;

AC P04953; 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 01-NOV-1991 (Rel. 20, Last annotation update)
 DE FIMBRIAL PROTEIN PRECURSOR (PILIN) (SEROGROUP H1) (265 ANTIGEN) (TWO SUBUNITS PILIN).
 GN FIMA.

OS Bacteroides nodosus (Dichelobacter nodosus).
 OC Bacteria; Proteobacteria; gamma subdivision; Cardiobacteriaceae;
 OC Dichelobacter.

OX NCBI_TaxID=870;

AC P04953; 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 01-NOV-1991 (Rel. 20, Last annotation update)
 DE FIMBRIAL PROTEIN PRECURSOR (PILIN) (SEROGROUP H1) (265 ANTIGEN) (TWO SUBUNITS PILIN).
 GN FIMA.

OS Bacteroides nodosus (Dichelobacter nodosus).
 OC Bacteria; Proteobacteria; gamma subdivision; Cardiobacteriaceae;
 OC Dichelobacter.

This SWISS-PROT entry is copyright. It is produced through a collaboration

```
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation at its CC CC CC European Bioinformatics Institute. There are no restrictions on its CC CC use by non-profit institutions as long as its content is in no way CC modified and this statement is not removed. Usage by and for commercial CC entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M26980; AAA23336.1; .
DR PIR; A37167; A37167.
DR HSSP; Q53391; IKB8.
DR InterPro; IPRO01082; Pilin.
DR InterPro; IPRO01120; Prok_N_methyltn.
DR Pfam; PF00114; pilin; 1.
DR PRODOM; PD000665; pilin; 1.
DR PROSITE; PS00409; PROKAR_NTERT_METHYL_1.
KM Fibbria; Methylation.
FT PROPEP 1
FT CHAIN 8 160 FIBRIAL PROTEIN.
FT MOD_RES 8 8 METHYLATION (BY SIMILARITY).
SO SEQUENCE 160 AA; 17169 MW; 3160DAEAE87ABA CRC64;
Query Match 20.8%; Score 133.5; DB 1; Length 160;
Best Local Similarity 27.8%; Pred. No. 0.0001;
Matches 37; Conservative 22; Mismatches 45; Indels 29; Gaps 4;
DY 8 ARQVTRAVSEVSALKTAESAILEGKEIVSAPPKRDYDIGTSTLLDGGSKSQIO- 66
DI:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 36 ARSGVRSMVESLGMRRAIEFCLLDGK-----KADECFIGWTKSNLGSASSPN 87
DY 67 ---VDNKK---DGVELVATLTGSSSAIKGAVITYSRKNDGWNNCKIIRT 111
DB 88 DSTADHPQGGLVIDYKLLEADATNAITVFQGNAAATLGRALKMTRPDKATWSCS---- 143
DY 112 PTAMKPNYAPANC 124
DB |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 144 -TDVELMKRPRPGC 155
RESULT 9
ECBP_EIKCO STANDARD; PRT; 159 AA.
AC P35646;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE FIBBRIAL PROTEIN ECBP PRECURSOR (PILIN).
GN ECBP.
OS Eikenella corrodens.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Eikenella.
OX NCBI_TaxID=539;
RN [1]
RS SEQUENCE FROM N.A.
RX SPRATN-ARC2 23834;
RX MEDLINE=93232782; PubMed=8473871;
RA Rao V.K.; Pirogulske-Fox A.;
RT "Cloning and sequencing of two type 4 (N-methylphenylalanine) pilin genes from Eikenella corrodens."
RL J. Gen. Microbiol. 139:651-660(1993).
CC -! SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration CC CC between the Swiss Institute of Bioinformatics and the EMBL Outstation - CC CC the European Bioinformatics Institute. There are no restrictions on its CC CC use by non-profit institutions as long as its content is in no way CC modified and this statement is not removed. Usage by and for commercial CC entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z12609; CAA78251.1; -.
DR PIR; S23845; S23845.
DR PIR; B47699; B47699.
DR HSSP; P02974; IAI12.
```

DR InterPro: IPR001082; PiliN.
 DR InterPro: IPR001120; Prok_N_methyltn.
 DR Pfam: PF00114; PiliN; 1.
 DR ProDom: PD000666; PiliN; 1.
 DR PROSITE: PS00409; PROKAR_NTER_METHYL; 1.
 KW Fimbria; Methylation.
 FT PROPEP 1 6 POTENTIAL.
 FT CHAIN 7 159 FIMBRIAL PROTEIN ECGB.
 FT MOD_RES 7 7 METHYLATION (BY SIMILARITY).
 FT DISULFID 137 156 BY SIMILARITY.
 SQ SEQUENCE 159 AA; 17387 MW; B6D5E3CF9183A90 CRC64;

Query Match 20.6%; Score 132.5; DB 1; Length 159;
 Best Local Similarity 30.7%; Pred. No. 0.00013;
 Matches 39; Conservative 17; Mismatches 56; Indels 15; Gaps 3;

QY 8 ARQVTVRAVEVSALKTAEASAI--LGKEIV--SSATPKDQYDIFGFTSTLLDGSQK---64
 DB 35 AKQINRVFELGSTRVAESILAHG----GIPYDPSQDGVVQSRRLRFLGLNQNRN 89
 QY 65 ----IQVTNKGTVLVAATLGKSSGSAIKGAVTVSRKNDGVWVCKITKTPAM-KP 117
 DB 90 SNLIFASVGLNSQPERVATFGNALPQIQGAVISFVNDQGWTCEDKSNAYCDP 149
 QY 118 NTAAPANC 124
 DB 150 KYPATC 156

RESULT 10
 FMCD_PSEAE STANDARD: PRT; 150 AA.
 AC P17837;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE FIMBRIAL PROTEIN PRECURSOR (PILIN) (STRAIN CD).
 GN PILA OR FIWA.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CD;
 RA MEDLINE=88138467; PubMed=2893774;
 RA Pasloske B.L., Joffe A.M., Sun O., Volpel K., Paranchych W.,
 RA Eftekhari F., Speert D.P.;
 RT "Serial isolates of Pseudomonas aeruginosa from a cystic fibrosis
 patient have identical pilin sequences.";
 RL Infect. Immun. 56:665-672(1988).
 CC -1- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
 NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
 CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
 CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.
 CC -1- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY. ALMOST IDENTICAL
 TO PA103 PILIN.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DR EMBL: M24281; AAA25945.1; ALT_INIT.
 DR PIR: A43504; A43504.
 DR HSP: P02973; INIL.
 DR InterPro: IPR001082; PiliN.
 DR InterPro: IPR001120; Prok_N_methyltn.
 DR Pfam: PF00114; PiliN; 1.

DR ProDom: PD000666; PiliN; 1.
 DR PROSITE: PS00409; PROKAR_NTER_METHYL; 1.
 KW Fimbria; Methylation.
 FT PROPEP 1 6
 FT CHAIN 7 150 FIMBRIAL PROTEIN.
 FT MOD_RES 7 7 METHYLATION (BY SIMILARITY).
 FT DISULFID 134 147 BY SIMILARITY.
 SQ SEQUENCE 150 AA; 15743 MW; E14316996F270F3C CRC64;

Query Match 18.8%; Score 121; DB 1; Length 150;
 Best Local Similarity 28.7%; Pred. No. 0.0011;
 Matches 35; Conservative 26; Mismatches 47; Indels 14; Gaps 6;

QY 8 ARQVTVRAVEVSALKTAEASAI--LGKEIV--SSATPKDQYDIFGFTSTLLDGSQK 62
 DB 35 ASSEASALATINPLKTVESLSKIGSKILIGTASTADTVY-VDIDKA--NKIGT 91
 QY 63 SQIQVTNKGTVLVAATLGKSSGSAIKGAVTVSRKNDGVWVCKITKTPAMKNVAPA 122
 DB 92 VAVTIKDGTVKFTFATGQSSPKN-AGKEITLNKTAEGVWTCSTQ-----EMFTPK 145
 QY 123 NC 124
 DB 146 GC 147

RESULT 11
 FMCD_PSEAE STANDARD: PRT; 150 AA.
 AC P08015;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE FIMBRIAL PROTEIN PRECURSOR (PILIN) (STRAIN PA103).
 GN PILA OR FIWA.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PA103;
 RA MEDLINE=87057209; PubMed=2430961;
 RA Johnson K., Parker M.W., Lory S.;
 RT "Nucleotide sequence and transcriptional initiation site of two
 Pseudomonas aeruginosa pilin genes.";
 RL J. Biol. Chem. 261:15703-15708(1986).
 CC -1- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
 NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
 CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
 CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.
 CC -1- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY. ALMOST IDENTICAL
 TO CD1 PILIN.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DR EMBL: M14850; AAA25933.1; -
 DR PIR: B24603; B24603.
 DR HSP: P02973; INIL.
 DR InterPro: IPR001082; PiliN.
 DR InterPro: IPR001120; Prok_N_methyltn.
 DR Pfam: PF00114; PiliN; 1.
 DR ProDom: PD000666; PiliN; 1.
 DR PROSITE: PS00409; PROKAR_NTER_METHYL; 1.
 KW Fimbria; Methylation.
 FT PROPEP 1
 DB 6

FT CHAIN 7 150 FIMBRIAL PROTEIN.
 MOD_RES 7 METHYLATION (BY SIMILARITY).
 FT DISULFID 134 147 BY SIMILARITY.
 SQ SEQUENCE 150 AA; 15799 MW; D8DAE68453D4DC85 CRC64;

Query Match 18.2%; Score 117; DB 1; Length 150;
 Best Local Similarity 27.9%; Pred. No. 0.0024;
 Matches 34; Conservative 27; Mismatches 47; Indels 14; Gaps 6;

QY 8 ARQGVRAVSEVSAIKTAAESAI--LEGEIY--SSAPKPDYDYGFTSTLLDSSGK 62
 Db 35 ARBEGSALATINPLKTYVESLSRGIAGSKILIGTASTADTTY-VGIDEKA--NKLGT 91
 Db 92 VAVTIKDTGDTIKFNATGSSPKN-AGREITLNRFAECVWCTSTQ-----EEMTPK 145
 QY 123 NC 124
 Db 146 GC 147

RESULT 12
 FMPO_PSEAE STANDARD; PRT; 149 AA.
 AC P04739;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE FIMBRIAL PROTEIN PRECURSOR (PILIN) (STRAIN PAO).
 GN PILA OR FIMA OR PA4525.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 NX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PAO;
 RX MEDLINE=86033611; PubMed=2997119;
 RA Sastiy P.A., Finlay B.B., Pasloske B.L., Paranchych W.,
 RA Pearstone J.R., Smillie L.B.;
 RT "Comparative studies of the amino acid and nucleotide sequences of
 RT pilin derived from Pseudomonas aeruginosa PAK and PAO.";
 RL J. Bacteriol. 164:571-577(1985).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 15692 / PAO1;
 RX MEDLINE=20437337; PubMed=10984043;
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
 RA Hickey M.J., Brinkman F.S.L., Huftagle W.O., Kowalik D.J., Lagrou M.,
 RA Gardner R.L., Goltz L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Laidig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
 RT "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
 RT opportunistic pathogen.";
 RL Nature 406:959-964(2000).
 RN [3]
 RP MUTAGENESIS OF GLU-11.
 RX MEDLINE=93321167; PubMed=8330261;
 RA Macdonald D.L., Pasloske B.L., Paranchych W.;
 RT "Mutations in the fifth-position glutamate in Pseudomonas aeruginosa
 RT pilin affect the transmethylation of the N-terminal phenylalanine.";
 RL Can. J. Microbiol. 39:500-505(1993).
 RN [4]
 RP STRUCTURE BY NMR OF 132-149.
 RX MEDLINE=96110702; PubMed=8845350;
 RA Campbell A.P., McInnes C., Hodges R.S., Sykes B.D.;
 RT "Comparison of NMR solution structures of the receptor binding
 RT domains of Pseudomonas aeruginosa pilin strains PAO, KB7, and PAK:
 RT implications for receptor binding and synthetic vaccine design.";
 RL Biochemistry 34:16255-16268(1995).

CC -1- SUBUNIT. THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
 CC NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
 CC CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
 CC CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.
 CC -1- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb.sib.ch/announce/>
 CC or send an email to license@isb.sib.ch).
 CC -----
 CC EMBL: M11323; AAA25954.1; -
 CC EMBL: AE004866; AAG07913.1; -
 CC PIR: A25023; A25023.
 CC PDB: 1P9N; 29-JAN-96.
 CC PDB: 1PAO; 29-JAN-96.
 CC InterPro: IPR001082; Pilin.
 CC InterPro: IPR001120; Prok_N_methyltn.
 CC Pfam: PF00114; Pilin; 1.
 CC ProDom: PD000666; Pilin; 1.
 CC DR PROSITE: PS00409; PROKAR_NTER_METHYL; 1.
 CC KEGG: Fimbrtia; Methylation; 3D-structure; Complete proteome.
 CC FT PROPEP 1 6
 CC FT CHAIN 7 149 FIMBRIAL PROTEIN.
 CC FT MOD_RES 7 7 METHYLATION (BY SIMILARITY).
 CC FT DISULFID 134 147 BY SIMILARITY.
 CC FT MTGAGEN 11 11 E->A: METHYLATION OF PHE-7 DECREASED AND
 CC FT LOSS OF PILI ASSEMBLY.
 CC SQ SEQUENCE 149 AA; 15512 MW; 98EC8A6F7B022214 CRC64;

Query Match 17.4%; Score 112; DB 1; Length 149;
 Best Local Similarity 29.2%; Pred. No. 0.0062;
 Matches 38; Conservative 19; Mismatches 47; Indels 26; Gaps 6;

QY 8 ARQGVRAVSEVSAIKTAAESAILLEGEIYSSATPKPDYDYGFTSTLLD----- 58
 Db 35 ARBEGSALATINPLKTYVESLSRG-----KIKIGTASTATETTYGVERDA 86
 QY 59 -GSKSQIQVTDKNDGVELVATIGKSS-GSAIGAVITYSRKNDGYWCKITTPPAWK 116
 Db 87 NKLGVIAVAIEDSGAGDITTFPGTSSPKNATK-VITLNRADGWACKSTODPM--- 141
 QY 117 PNYPANCPN 126
 Db 142 --FTPKGCDN 149

RESULT 13
 FMPO_PSEAE STANDARD; PRT; 150 AA.
 AC P02973; O53390.
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE FIMBRIAL PROTEIN PRECURSOR (PILIN) (STRAIN PAK).
 GN PILA OR FIMA.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 NX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PAK;
 RX MEDLINE=85180008; PubMed=2985436;
 RA Pasloske B.L., Finlay B.B., Paranchych W.;
 RT "Cloning and sequencing of the Pseudomonas aeruginosa PAK pilin
 RT gene.";
 RL FEBS Lett. 183:408-412(1985).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN-PAK;
 RX MEDLINE=87057209; PubMed=2430961;
 RA Johnson K, Parker M.L., Lory S.;
 RT "Nucleotide sequence and transcriptional initiation site of two
 pseudomonas aeruginosa pilin genes.";
 RN J. Biol. Chem. 261:15703-15708(1986).
 RP SEQUENCE OF 7-150.
 RC STRAIN-PAK;
 RX MEDLINE=83158129; PubMed=6131838;
 RA Saez P.A., Pearlstone J.R., Smillie L.B., Paranchych W.;
 RT "Amino acid sequence of pilin isolated from pseudomonas aeruginosa
 PAK.";
 RN FEBS Lett. 151:253-256(1983).
 RP SEQUENCE OF 128-150 FROM N.A.
 RX MEDLINE=94103636; PubMed=7903973;
 RA IPATSG;
 RT "A multicenter comparison of methods for typing strains of
 pseudomonas aeruginosa predominantly from patients with cystic
 fibrosis. The International Pseudomonas aeruginosa Typing Study
 Group.";
 RN J. Infect. Dis. 169:134-142(1994).
 RP STRUCTURE BY NMR OF 134-150.
 RX MEDLINE=94079874; PubMed=8257679;
 RA McInnes C., Soenichsen F.D., Kay C.M., Hodges R.S., Sykes B.D.;
 RT "NMR solution structure and flexibility of a peptide antigen
 representing the receptor binding domain of Pseudomonas aeruginosa.";
 RN Biochemistry 32:13432-13440(1993).
 CC -1- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
 NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
 CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
 CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILIUS.
 CC -1- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@sib-sib.ch).
 CC EMBL: M14849; AAA25955.1;
 DR EMBL: X02402; CAA26248.1;
 DR EMBL: S67807; CAB32859.1;
 DR PIR: A03497; YOPSPA.
 DR PIR: A24603; A24603.
 DR PIR: A28780; A28780.
 DR PDB: 1PAU; 31-JAN-94.
 DR PDB: 1PAK; 31-JAN-94.
 DR PDB: 1NIL; 29-JAN-96.
 DR PDB: 1NIM; 29-JAN-96.
 DR InterPro: IPR001082; pilin.
 DR InterPro: IPR001120; Prok_N_methyltn.
 DR Pfam: PF00114; pilin; 1.
 DR ProDom: PD000666; pilin; 1.
 DR PROSITE: PS00409; PROKAR_NTER_METHYL; 1.
 KW Fimbria; Methylation; 3D-structure.
 FT PROPEP 1 6
 FT CHAIN 7 150
 FT MOD_RES 7 150 FIMBRIAL PROTEIN.
 FT DISULFID 135 148 METHYLATION (BY SIMILARITY).
 FT CONFLICT 90 90 T -> TS (IN REF. 3).
 FT CONFLICT 101 103 TAD -> DTA (IN REF. 3).
 FT CONFLICT 128 128 A -> D (IN REF. 4).
 FT CONFLICT 150 150 R -> K (IN REF. 2).
 SO SEQUENCE 150 AA; 15650 MW; C0E35B69FD6FBE84 CRC64;

Query Match

15.4%; Score 99; DB 1; Length 150;

Best Local Similarity 30.8%; Pred. No. 0.076;
 Matches 33; Conservative 19; Mismatches 41; Indels 14; Gaps 6;
 QY 8 ARNQVTRAVESEVSAALKTAESAALLEKEIVS-----SAPPKDTQVDIGFTSTLLDGSGK 62
 DB 35 ARSEGASALASVNPPLKTYVEALSRGWSVSGTGTEADATRKVEPLGVADANKL-----CT 90
 QY 63 SQIQVTDNKDGT--VELVATLKGSSAIGAVITVSR-KNDGVNVC 106
 DB 91 IALK-BDPPADGTADITLFTFMG-GAGPKKKKGIITITRTAAGMKC 135
 RESULT 14
 FMZD_BACNO
 ID FMZD_BACNO STANDARD; PRT; 159 AA.
 AC P17416;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE POSSIBLE MINOR FIMBRIAL PROTEIN PRECURSOR (PILIN) (SEROGROUP D).
 GN FIMZ.
 OS Bacteroides nodosus (Dichelobacter nodosus).
 OC Bacteria; Proteobacteria; gamma subdivision; Cardiobacteriaceae;
 OC Dichelobacter.
 OX NCBI_TaxID=870;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SEROGROUP D ISOLATE VCS1172;
 RX MEDLINE=91260439; PubMed=1675418;
 RA Hobbs M., Dairymple B.P., Cox P.T., Livingstone S.P., Delaney S.F.,
 RA Maltick J.S.;
 RT "Organization of the fimbrial gene region of Bacteroides nodosus:
 class I and class II strains.";
 RN Mol. Microbiol. 5:543-560(1991).
 CC -1- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
 NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
 CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
 CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILIUS.
 CC -1- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@sib-sib.ch).
 CC EMBL: X52389; -; NOT_ANNOTATED_CDS.
 DR PIR: S15249; YOBZDZ.
 DR HSSP: P02974; IAYZ.
 DR InterPro: IPR001082; pilin.
 DR InterPro: IPR001120; Prok_N_methyltn.
 DR Pfam: PF00114; pilin; 1.
 DR ProDom: PD000666; pilin; 1.
 DR PROSITE: PS00409; PROKAR_NTER_METHYL; 1.
 KW Fimbria; Methylation.
 FT PROPEP 1 6
 FT CHAIN 7 159
 FT MOD_RES 7 159 POSSIBLE MINOR FIMBRIAL PROTEIN.
 FT DISULFID 56 71 METHYLATION (BY SIMILARITY).
 FT DISULFID 140 153 BY SIMILARITY.
 SO SEQUENCE 159 AA; 17102 MW; E53B80EC52B86C82 CRC64;

Query Match

Best Local Similarity 15.3%; Score 98; DB 1; Length 159;

Matches 30; Conservative 19; Mismatches 59; Indels 18; Gaps 3;

QY 9 RTQVTRAVESEVSAALKTAESAALLEKEIVSAPPKDTQVDIGFTSTLLDGSGKSOIQVY 68
 DB 36 RSOVTRVLMAGELRLAVELCNDLGDITTVGNGA---NECDPRASGSGNITISGASQNEIYI 92

QY 69 DNKGTYE-----LVATLGSSGSAIKGAVITVSRKNDGVWCKITKPTANKPN 118
 Db 93 AANTGVQFPNPLTEETALTATENNSAASIIHGKLIWQKSGSWYCHSNA-----EK 147
 QY 119 YAPANC 124
 Db 148 FLPSGC 153

RESULT 15

FMNC_PSEPU

ID FMNC_PSEPU

AC P36643

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DE FIMBRIAL PROTEIN PRECURSOR (PILIN).

GN PILA.

OS Pseudomonas putida.

OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;

OC Pseudomonas.

OX NCBI_TaxID=303;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=MCS358;

RX MEDLINE=94131942; PubMed=7905475;

RA de Groot A., Heljnen T., de Cock H., Filloux A., Tomassen J.;

RT "Characterization of type IV pilus genes in plant growth-promoting

Pseudomonas putida WCS358."

J. Bacteriol. 176:642-650(1994).

CC -1- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

Query Match 15.08; Score 96; DB 1; Length 136;
 Best Local Similarity 26.08; Pred. No. 0.12;
 Matches 32; Conservative 21; Mismatches 40; Indels 30; Gaps 6;

QY 8 ARTGVTRAVSEVSAIKTAESAILEGKEIVSAPKDTQYDIG-----FTESTLLOSG 61
 Db 35 SRTYAAAGLEISALKTAMDRLNEGKDA-----DVGALGGOPATAHCAITASG 84
 QY 62 KSOIQVTDNKTVELVATLGSSGSAIKGAVITVSRKNDGVWCKITKPTANKPNYAP 121
 Db 85 NAAA-----GTGSIYCTLVADAPATYV--GKALILITRATG--WGC-----TTNIEDLAP 130
 QY 122 ANC 124
 Db 131 SGC 133

Search completed: February 8, 2002, 15:34:23
 Job time: 548 sec

Fri Feb 8 15:44:57 2002

us-09-865-159-8.rsp

Page 10

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 8, 2002, 15:33:54 ; Search time 67.44 Seconds

(without alignments)
275,454 Million cell updates/sec

Title: US-09-865-159-8

Perfect score: 642

Sequence: 1 ALEGTETPRTQVTRAVSEVS.....ITKTPPAKPNVAPANCPS 127

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 473505 segs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPREMBL.17:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.podent:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	521	81.2	154	2	059794 pseudomonas
2	194.5	30.3	156	2	059508 moraxella b
3	188.5	29.4	157	2	059503 moraxella b
4	181	28.2	156	2	059507 moraxella b
5	180.5	28.1	159	2	060163 moraxella b
6	164	25.5	160	2	059504 moraxella b
7	160.5	25.0	131	2	09AP36 bacteroides
8	160.5	25.0	157	2	059336 dichelobact
9	158.5	24.7	159	2	059505 moraxella b
10	151	23.5	158	2	059501 moraxella b
11	138.5	21.6	143	2	048936 moraxella b
12	133.5	20.8	134	2	09S4E1 bacteroides
13	131	20.4	130	2	09S4E2 bacteroides
14	129	20.1	136	2	056799 xanthomonas
15	116	18.1	130	2	09AP34 xanthomonas
16	115	17.9	145	2	09APK5 xanthomonas
17	115	17.9	146	2	052613 xanthomonas
18	112.5	17.5	139	2	09ZEL3 pseudomonas
19	109	17.0	150	2	059795 pseudomonas

20	108.5	16.9	148	2	09PAH9 xylella fas
21	107.5	16.7	116	2	09APJ3 xanthomonas
22	102	15.9	29	2	053393 pseudomonas
23	102	15.9	135	2	056800 xanthomonas
24	96.5	15.0	140	2	09F671 pseudomonas
25	89	13.9	24	2	053392 pseudomonas
26	86.5	13.5	1576	10	09RCX4 arabisopsis
27	85	13.2	692	2	053922 staphylococ
28	85	13.2	1051	10	09LXN4 arabisopsis
29	84.5	13.0	675	2	057071 staphylococ
30	83.5	13.0	273	2	044676 borrelia af
31	83	12.9	525	5	021205 ceenorhabdi
32	83	12.9	534	5	09XV7 ceenorhabdi
33	82.5	12.9	241	2	053831 spiroplasma
34	82.5	12.9	242	2	053830 spiroplasma
35	81.5	12.7	241	2	053828 spiroplasma
36	81.5	12.7	241	2	057034 spiroplasma
37	81.5	12.7	762	2	09A7G7 caulobacter
38	81	12.6	553	5	015820 entamoeba h
39	81	12.6	553	5	018719 entamoeba d
40	80.5	12.5	277	2	0927B2 chlamydia p
41	79.5	12.4	241	2	053829 spiroplasma
42	79.5	12.4	254	2	054320 borrelia af
43	79.5	12.4	273	2	044956 borrelia bu
44	79.5	12.4	273	2	044950 borrelia bu
45	79.5	12.4	273	2	044974 borrelia bu

ALIGNMENTS

RESULT 1
ID 059794 PRELIMINARY; PRT; 154 AA.
AC 059794;
DT 01-JUN-1998 (TREMblrel. 06, Created)
DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE FIMBRIAL PROTEIN PRECURSOR (PILIN) (STRAIN 57/B).
GN PILA OR FIMA.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=57/B;
RX MEDLINE=94131566; PubMed=7507890;
RA Castic P.A., Deal C.D.;
RT "Differentiation of Pseudomonas aeruginosa pilI based on sequence and B-cell epitope analyses";
RL Infect. Immun. 62:371-376(1994).
CC -I- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4 NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.
CC -I- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
DR EMBL; S68101; AAC60461.1; -;
DR HSSP; P02974; 2PIL.
DR InterPro; IPR001082; Pilin.
DR InterPro; IPR001120; Prok_N_methyltn.
DR Pfam; PF00114; Pilin; 1.
DR ProDom; PD000666; Pilin; 1.
DR PROSITE; PS00409; PROKAR_NTER_METHYL. 1.
KW Fimbria; Methylation.
FT PROPEP 1
FT CHAIN 7 154 FIMBRIAL PROTEIN.
FT DISULFD 133 151 BY SIMILARITY.
FT MOD_RES 7 METHYLATION (BY SIMILARITY).
SQ SEQUENCE 154 AA; 16317 MW; 5240A56725155719 CRC64;

Query Match 81.2%; Score 521; PB 2; Length 154;

DR EMBL; M92155; AA

OC Bacteria; Proteobacteria; gamma subdivision; Cardiobacteriaceae;
 OC Dichelobacter.
 OC NCBI_TaxID=870;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhou H., Hickford J.G.H.;
 RT "Dichelobacter nodosus fimbrial subunit gene";
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF316610; AAK00323.1;
 FT NON_PRR 1
 SQ SEQUENCE 131 AA; 13933 MW; 546D620DCECB1ABD CRC64;

Query Match 25.0%; Score 160.5; DB 2; Length 131;
 Best Local Similarity 31.6%; Pred. No. 3.4e-07;
 Matches 42; Conservative 24; Mismatches 36; Indels 31; Gaps 5;

QY 8 ARQVTRAVSEVSAALTAESAILEGKEIVSSATPKDYOYDIGFTSTLLDG----- 59
 DB 10 ARSQVSRVMSSETGOMRTALETCVLDGKEA-----DKCFIGWTSNLLDGEFTAGTES 61
 QY 60 ----SGKSQI----QVTDNKDGTVELVATLGKSSGSAIKGAVITVSRKNDGVWNCKITRT 111
 DB 62 TAAATGQTGITTKYPVAADDEGNI--VATFGNMAAAIKPQTLTWSRSKEGTWC----- 114
 QY 112 PTAMKPNVAPANC 124
 DB 115 ATTVEAKFOPTGC 127

RESULT 8
 Q59336 PRELIMINARY; PRT; 157 AA.
 ID 059336;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE PILIN
 OS Dichelobacter nodosus H1.
 OC Bacteria; Proteobacteria; gamma subdivision; Cardiobacteriaceae;
 OC Dichelobacter.
 OX NCBI_TaxID=46911;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BN265;
 RX MEDLINE=90155189; PubMed-2621448;
 RA Hoyle P.A., Elleman T.C., McKern N.M., Stewart D.J.;
 RT "Sequence of pilin from Bacteroides nodosus 351 (Serogroup H) and
 RL implications for serogroup classification.";
 RL J. Gen. Microbiol. 135:1113-1122(1989)
 CC -1- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
 CC NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
 CC CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
 CC CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE FIMBRIAL PROTEIN (N-ME-PHE)PILIN
 CC FAMILY.
 CC EMBL: M26979; AAA98742.1;
 DR HSP: Q53391; 1KB8
 DR InterPro: IPR001082; Pilin.
 DR InterPro: IPR001120; Prok_N_methyltn.
 DR Pfam: PF00114; Pilin; 1.
 DR ProDom: PD000666; Pilin; 1.
 DR PROSITE: PS00409; PROKAR_NTER_METHYL; 1;
 KW Fimbria; Methylation.
 FT MOD_RES 8
 SQ SEQUENCE 157 AA; 16702 MW; 63E01952511E0967 CRC64;

Query Match 25.0%; Score 160.5; DB 2; Length 157;
 Best Local Similarity 31.6%; Pred. No. 4.3e-07;
 Matches 42; Conservative 24; Mismatches 36; Indels 31; Gaps 5;

QY 8 ARTQVTRAVSEVSAALTAESAILEGKEIVSSATPKDYOYDIGFTSTLLDG----- 59
 DB 36 ARSQVSRVMSSETGOMRTALETCVLDGKEA-----DKCFIGWTSNLLDGEFTAGTES 87
 QY 60 ----SGKSQI----QVTDNKDGTVELVATLGKSSGSAIKGAVITVSRKNDGVWNCKITRT 111
 DB 88 TAAATGQTGITTKYPVAADDEGNI--VATFGNMAAAIKPQTLTWSRSKEGTWC----- 140
 QY 112 PTAMKPNVAPANC 124
 DB 141 ATTVEAKFOPTGC 153

RESULT 9
 Q59505 PRELIMINARY; PRT; 159 AA.
 ID 059505;
 AC 059505;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE PREPILIN.
 OS Moraxella bovis.
 OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae; Moraxella.
 OX NCBI_TaxID=476;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TAT849 / SEROGROUP E;
 RX MEDLINE=94327452; PubMed-8051000;
 RA Atwell J.L., Tennent J.M., Lepper A.W., Elleman T.C.;
 RT "Characterization of pilin genes from seven serologically defined
 RT prototype strains of Moraxella bovis.";
 RL J. Bacteriol. 176:4875-4882(1994).
 CC -1- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
 CC NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
 CC CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
 CC CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE FIMBRIAL PROTEIN (N-ME-PHE)PILIN
 CC FAMILY.
 CC EMBL: L32972; AAA53561.1;
 DR InterPro: IPR001082; Pilin.
 DR InterPro: IPR001120; Prok_N_methyltn.
 DR Pfam: PF00114; Pilin; 1.
 DR ProDom: PD000666; Pilin; 1.
 DR PROSITE: PS00409; PROKAR_NTER_METHYL; 1.
 KW Fimbria; Methylation.
 FT MOD_RES 7
 SQ SEQUENCE 159 AA; 16534 MW; F40828A90E93089 CRC64;

Query Match 24.7%; Score 158.5; DB 2; Length 159;
 Best Local Similarity 30.5%; Pred. No. 6.6e-07;
 Matches 40; Conservative 24; Mismatches 44; Indels 23; Gaps 3;

QY 8 ARTQVTRAVSEVSAALTAESAILEGKEIVSSATPKDYOYDIGFT-----ES 54
 DB 35 SKSQTRVAVGELACGTAVADALFECKRTVLEASTSKENIGLTTSENSATPRSNLMES 94
 QY 55 TLDDGSKSQIOYTDNKDGTVELVATLGKSSGSAIKGAVITVSRKNDGVWNCKITRT 113
 DB 95 VSLEGF-----DSNQGGSISATLGNANAKDIKAVISQNRRTDGVWNCCEVNGKAP 145
 QY 114 AMKPNVAPANC 124
 DB 146 KYKAFTPAGC 156

RESULT 10
 Q59501 PRELIMINARY; PRT; 158 AA.
 ID 059501;
 AC 059501;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DT 01-JUN-2001 (Tremblrel. 17, last annotation update)
 DE PREPILIN.
 OS Moraxella bovis.
 OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae; Moraxella.
 ON NCBI_TaxID=476;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=218 / SEROGROUP F;
 RX MEDLINE=94327452; PubMed=8051000;
 RA Atwell J.L., Tennent J.M., Lepper A.W., Elleman T.C.;
 RT "characterisation of pilin genes from seven serologically defined
 RT prototype strains of Moraxella bovis."
 RU J. Bacteriol. 176:4875-4882(1994).
 CC -1- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
 CC NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
 CC CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
 CC CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PLUS (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE FIMBRIAL PROTEIN (N-HE-PHE)PILIN
 CC FAMILY.
 CC EMBL: L32965; AAA5356.1; .
 DR InterPro: IPR001082; Pili.
 DR InterPro: IPR001120; Prok_N_methyltn.
 DR Pfam: PF00114; Pili; 1.
 DR ProDom: PD000666; Pili; 1.
 DR PROSITE: PS00409; PROKAR_NTER_METHYL; 1.
 KW Fimbria; Methylation.
 FT MOD_RES 7
 SQ SEQUENCE 158 AA; 16216 MW; 620B513CA4DC39A5 CRC64;

Query Match 23.5%; Score 151; DB 2; Length 158;
 Best Local Similarity 31.5%; Pred. No. 3; Le-06;
 Matches 39; Conservative 21; Mismatches 54; Indels 10; Gaps 3;

QY 8 ARQVTRAVSEVSALKTAAESAILLEGKEIVSSATPKDYOYDYGTESTLLDGSQKQIQ 67
 ID Q48936 PRELIMINARY; PRT; 143 AA.
 AC Q48936;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, last annotation update)
 DE PILIN (FRAGMENT).
 OS Moraxella bovis.
 OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae; Moraxella.
 ON NCBI_TaxID=476;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=D2D SEROGROUP C;
 RX MEDLINE=94327452; PubMed=8051000;
 RA Atwell J.L., Tennent J.M., Lepper A.W., Elleman T.C.;
 RT "characterisation of pilin genes from seven serologically defined
 RT prototype strains of Moraxella bovis."
 RU J. Bacteriol. 176:4875-4882(1994).
 CC EMBL: L32967; AAA5356.1; .
 DR InterPro: IPR001082; Pili.
 DR Pfam: PF00114; Pili; 1.
 DR ProDom: PD000666; Pili; 1.
 FT NON_TER 143
 SQ SEQUENCE 143 AA; 15158 MW; F32PD85A6DB8D60C CRC64;

Query Match 21.6%; Score 138.5; DB 2; Length 143;
 Best Local Similarity 29.9%; Pred. No. 3; 7e-05;
 Matches 38; Conservative 24; Mismatches 50; Indels 15; Gaps 5;

QY 8 ARQVTRAVSEVSALKTAAESAILLEGKEIVSSATPKDYOYDYGTESTLLDGSQKQIQ 66
 ID Q9S4E1 PRELIMINARY; PRT; 134 AA.
 AC Q9S4E1;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, last annotation update)
 DE FIMBRIAL SUBUNIT (FRAGMENT).
 GN FIWA.
 OS Bacteroides nodosus (Dichelobacter nodosus).
 OC Bacteria; Proteobacteria; gamma subdivision; Cardiobacteriaceae;
 OC Dichelobacter.
 ON NCBI_TaxID=870;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhou H., Hickford J.G.H.;
 RT "Dichelobacter nodosus fimbrial subunit gene (fiwa)";
 RU Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF146891; AAD43068.1; .
 DR HSSP: Q53391; 1KB8.
 DR InterPro: IPR001082; Pili.
 DR Pfam: PF00114; Pili; 1.
 DR ProDom: PD000666; Pili; 1.
 FT NON_TER 1
 SQ SEQUENCE 134 AA; 14409 MW; EFB9AB2C330CF7E CRC64;

Query Match 20.8%; Score 133.5; DB 2; Length 134;
 Best Local Similarity 27.8%; Pred. No. 9; 5e-05;
 Matches 37; Conservative 22; Mismatches 45; Indels 29; Gaps 4;

QY 8 ARQVTRAVSEVSALKTAAESAILLEGKEIVSSATPKDYOYDYGTESTLLDGSQKQIQ 66
 ID Q9S4E2 PRELIMINARY; PRT; 130 AA.
 AC Q9S4E2;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, last annotation update)
 DE FIMBRIAL SUBUNIT (FRAGMENT).
 GN FIWA.
 OS Bacteroides nodosus (Dichelobacter nodosus).
 OC Bacteria; Proteobacteria; gamma subdivision; Cardiobacteriaceae;
 OC Dichelobacter.
 ON NCBI_TaxID=870;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhou H., Hickford J.G.H.;
 RT "Dichelobacter nodosus fimbrial subunit gene (fiwa)";
 RU Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF146891; AAD43068.1; .
 DR HSSP: Q53391; 1KB8.
 DR InterPro: IPR001082; Pili.
 DR Pfam: PF00114; Pili; 1.
 DR ProDom: PD000666; Pili; 1.
 FT NON_TER 1
 SQ SEQUENCE 134 AA; 14409 MW; EFB9AB2C330CF7E CRC64;

OC Bacteria; Proteobacteria; gamma subdivision; Cardiobacteriaceae;
 OC Dichelobacter.
 OX NCBI_TaxID=870;
 RN [1]
 RN SEQUENCE FROM N.A.
 RA Zhou H., Hickford J.G.H.;
 RT "Dichelobacter nodosus fimbrial subunit gene (fima).";
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Zhou H., Hickford J.G.H.;
 RT "Dichelobacter nodosus fimbrial subunit gene.;"
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF146890; AAD43087.1;
 DR EMBL; AF146891; AAD43088.1;
 DR InterPro: IPR001082; Pfam: PF00114; Pfam: PF00114; Pfam: PF00114;
 DR ProDom: PD000666; Pfam: 1.
 FT NON TER 1
 SO SEQUENCE 130 AA; 13838 MW; 0978D248FEA6C9D CRC64;

Query Match 20.4%; Score 131; DB 2; Length 130;
 Best Local Similarity 30.5%; Pred. No. 0.00015;
 Matches 39; Conservative 23; Mismatches 36; Indels 30; Gaps 6;

QY 8 ARTQVTRAVSEVSAKTAESAILEGKEIVSSATPKDQYDYGFTSTLLDSSGSKQIOV 67
 Db 10 AKSQVSRVSEVSGMTAETCTLDGKE-----GKDC--FLGWTSLNLAAGS---T 58
 QY 68 TDNR-----DGTVE--LVATLGKSSGSAIKGAVITVSRKNDGVNCKIT 109
 Db 59 TNNATADPGCGGLNATVALESTAEKTEATFGQNAATLHGKLTWTRSPATWCS-T 117
 QY 110 KPTTANKP 117
 Db 118 DVDEKFKP 125

RESULT 14
 ID 056799 PRELIMINARY; PRF; 136 AA.
 AC 056799;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE FIMBRILLIN.
 GN FIMA.
 OS Xanthomonas campestris.
 OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
 OX NCBI_TaxID=339;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SMPAIN-3240 (NCPB);
 RX MEDLINE=9717558; PubMed=9023213;
 RA Ojaneu-Reus T., Kalkinen N., Westerlund-wikstrom B., van Doorn J.,
 RA Haahela K., Nurmiho-lasala E.L., Wengelin K., Bonas U.,
 RA Korhonen T.K.;
 RT "Characterization of the fima gene encoding bundle-forming fimbriae of
 RT the plant pathogen Xanthomonas campestris pv. vesicatoria.";
 RL J. Bacteriol. 179:1280-1290(1997).
 DR EMBL; Z48759; CAA88680.1;
 DR InterPro: IPR001082; Pfam: PF00114; Pfam: PF00114;
 DR ProDom: PD000666; Pfam: 1.
 SO SEQUENCE 136 AA; 14302 MW; A834A9C4EA7C63B1 CRC64;

Query Match 20.1%; Score 129; DB 2; Length 136;
 Best Local Similarity 30.8%; Pred. No. 0.00025;
 Matches 37; Conservative 16; Mismatches 49; Indels 18; Gaps 3;

QY 8 ARTQVTRAVSEVSAKTAESAILEGKEIVSSATPKDQYDYGFTSTLLDSSGSKQIOV 67
 Db 35 AKSQVTRAVSEVSAKTAESAILEGKEIVSSATPKDQYDYGFTSTLLDSSGSKQIOV 67
 QY 68 TDNR-----DGTVE--LVATLGKSSGSAIKGAVITVSRKNDGVNCKITPTANKPNYAPANPN 127
 Db 84 TALSATGTIECTL--KNTQVVGKVKVTLFRANDGTWCK-----TDALKKTAAPACGCA 136

RESULT 15
 ID 09APJ4 PRELIMINARY; PRF; 130 AA.
 AC 09APJ4;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE TYPE 4 FIMBRILLIN SUBUNIT (FRAGMENT).
 OS Xanthomonas translucens pv. cerealis.
 OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
 OX NCBI_TaxID=152263;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=1157222;
 RA van Doorn J.J., Hollinger T.C., Oudega B.;
 RT "Analysis of the type IV fimbrial-Subunit Gene fima of Xanthomonas
 RT hyacinthi: Application in PCR-Mediated Detection of Yellow Disease in
 RT Hyacinths.";
 RL Appl. Environ. Microbiol. 67:598-607(2001).
 DR EMBL; AF282629; AAK1164.1;
 FT NON TER 1
 SO SEQUENCE 130 AA; 13291 MW; 2DB4BE6AB37C9D1D CRC64;

Query Match 18.1%; Score 116; DB 2; Length 130;
 Best Local Similarity 30.6%; Pred. No. 0.0034;
 Matches 37; Conservative 17; Mismatches 47; Indels 20; Gaps 5;

QY 8 ARTQVTRAVSEVSAKTAESAILEGKEIVSSATPKDQYDYGFTSTLLDSSGSKQIOV 67
 Db 23 AKSQVTRAVSEVSAKTAESAILEGKEIVSSATPKDQYDYGFTSTLLDSSGSKQIOV 67
 QY 68 TDNR-----DGTVE--LVATLGKSSGSAIKGAVITVSRKNDGVNCKITPTANKPNYAPAN 123
 Db 72 SVNPTGATLTCTLKGNAQTNGOATQWTRVADPANGNTGWTG-----TTAIVKLRPAT 126
 QY 124 C 124
 Db 127 C 127

Search completed: February 8, 2002, 15:33:54
 Job time: 359 sec

Fri Feb 8 15:44:57 2002

us-09-865-159-8.rspt

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 8, 2002, 15:25:11 ; Search time 32.48 Seconds
(Without alignments)
87.990 Million cell updates/sec

Title: US-09-865-159-8

Sequence: 1 ALEGTETPRTQVTRAVSEVS.....ITKPTANKPNTPANPCNS 127

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents, AA: *
1: /cgn2_6/prodata/2/1aa/5A.COMB.pep: *
2: /cgn2_6/prodata/2/1aa/5B.COMB.pep: *
3: /cgn2_6/prodata/2/1aa/5C.COMB.pep: *
4: /cgn2_6/prodata/2/1aa/5D.COMB.pep: *
5: /cgn2_6/prodata/2/1aa/5E.COMB.pep: *
6: /cgn2_6/prodata/2/1aa/5F.COMB.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	597	93.0	154	3	US-08-486-099-108
2	597	93.0	154	3	US-08-360-107A-118
3	597	93.0	154	3	US-08-484-223B-108
4	597	93.0	154	3	US-08-919-297-108
5	597	93.0	154	3	US-08-475-668A-108
6	597	93.0	154	3	US-08-485-551A-108
7	597	93.0	154	3	US-08-471-913A-108
8	597	93.0	154	4	US-08-485-264A-108
9	132	20.6	23	1	US-07-638-492-7
10	128	19.9	22	1	US-08-084-739-7
11	115	17.9	19	6	5445818-7
12	98	15.3	23	1	US-07-638-492-10
13	94	14.6	23	1	US-07-638-492-9
14	94	14.6	22	1	US-08-084-739-12
15	90	14.0	22	1	US-08-084-739-11
16	85	13.2	22	1	US-08-084-739-11
17	83	12.9	19	6	5445818-8
18	79.5	12.4	27	3	US-08-137-175A-5
19	79.5	12.4	27	4	US-08-479-017-5
20	79.5	12.4	27	4	US-09-196-293-13
21	79.5	12.4	27	3	US-08-209-603E-13
22	79.5	12.4	338	2	US-08-441-857-10
23	79.5	12.4	338	3	US-08-193-159-10
24	79.5	12.4	338	3	US-08-193-159-10
25	76.5	11.9	273	4	US-08-840-466A-19
26	76.5	11.9	273	4	US-08-235-836C-11
27	76.5	11.9	273	4	US-08-235-836C-89
					Sequence 89, Appl
					Sequence 140, App

ALIGNMENTS

28	76.5	11.9	314	1	US-08-040-753-2	Sequence 2, Appl
29	74.5	11.6	466	4	US-08-235-836C-110	Sequence 110, App
30	73	11.4	1912	1	US-08-409-995-4	Sequence 4, Appl
31	73	11.4	1912	3	US-08-685-467-4	Sequence 4, Appl
32	73	11.4	2353	4	US-09-377-155-33	Sequence 33, Appl
33	73	11.4	2353	4	US-08-913-942-4	Sequence 4, Appl
34	72	11.2	679	4	US-08-913-942-4	Sequence 15, Appl
35	71.5	11.1	273	4	US-08-235-836C-142	Sequence 142, App
36	71	11.1	338	2	US-08-441-857-12	Sequence 12, App
37	71	11.1	338	3	US-08-193-159-12	Sequence 12, Appl
38	71	11.1	1222	2	US-08-682-517-15	Sequence 15, Appl
39	71	11.1	1252	2	US-08-682-517-9	Sequence 9, Appl
40	70.5	11.0	526	2	US-08-853-659A-40	Sequence 40, Appl
41	70	10.9	274	2	US-08-441-857-2	Sequence 2, Appl
42	70	10.9	274	3	US-08-193-159-2	Sequence 2, Appl
43	70	10.9	339	2	US-08-441-857-6	Sequence 6, Appl
44	70	10.9	339	3	US-08-193-159-6	Sequence 6, Appl
45	69.5	10.8	279	4	US-09-097-767A-14	Sequence 14, Appl

RESULT 1

US-08-486-099-108
Sequence 108, Application US/08486099
Patent No. 6013263

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lamber, Dennis M.
APPLICANT: Peteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
TITLE OF INVENTION: B VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486, 099
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-031
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 108:

SEQUENCE CHARACTERISTICS:
LENGTH: 154 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-486-099-108

Query Match 93.0%; Score 597; DB 3; Length 154;
 Best Local Similarity 98.3%; Pred. No. 4.8e-60;
 Matches 118; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 ARTQVTRAVSEVSAIKTAESAILEGKEIVSSATPKDQYDYGFTSTLLDGSQSOIY 67
 DB 35 ARTQVTRAVSEVSAIKTAESAILEGKEIVSSATPKDQYDYGFTSTLLDGSQSOIY 94

QY 68 TNNKDGTVELVATLKGSSSAIKGAVITVSRKNDGVWNCITTKPTPAKPNYPANCPNS 127
 DB 95 TNNKDGTVELVATLKGSSSAIKGAVITVSRKNDGVWNCITTKPTPAKPNYPANCPNS 154

RESULT 2
 US-08-360-107A-118

; Sequence 118, Application US/08360107A
 ; Patent No. 6017536

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.
 APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petterway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION

TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV

NUMBER OF SEQUENCES: 149

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/360.107A

FILING DATE: 20-DEC-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-013

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 118:

SEQUENCE CHARACTERISTICS:

LENGTH: 154 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-08-360-107A-118

Query Match 93.0%; Score 597; DB 3; Length 154;
 Best Local Similarity 98.3%; Pred. No. 4.8e-60;
 Matches 118; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 ARTQVTRAVSEVSAIKTAESAILEGKEIVSSATPKDQYDYGFTSTLLDGSQSOIY 67
 DB 35 ARTQVTRAVSEVSAIKTAESAILEGKEIVSSATPKDQYDYGFTSTLLDGSQSOIY 94

QY 68 TNNKDGTVELVATLKGSSSAIKGAVITVSRKNDGVWNCITTKPTPAKPNYPANCPNS 127
 DB 95 TNNKDGTVELVATLKGSSSAIKGAVITVSRKNDGVWNCITTKPTPAKPNYPANCPNS 154

DB 95 TNNKDGTVELVATLKGSSSAIKGAVITVSRKNDGVWNCITTKPTPAKPNYPANCPNS 154

RESULT 3
 US-08-484-223B-108

; Sequence 108, Application US/08484223B
 ; Patent No. 6020459

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petterway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF

TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV

NUMBER OF SEQUENCES: 245

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/484.223B

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-029

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 108:

SEQUENCE CHARACTERISTICS:

LENGTH: 154 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-08-484-223B-108

Query Match 93.0%; Score 597; DB 3; Length 154;
 Best Local Similarity 98.3%; Pred. No. 4.8e-60;
 Matches 118; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 ARTQVTRAVSEVSAIKTAESAILEGKEIVSSATPKDQYDYGFTSTLLDGSQSOIY 67
 DB 35 ARTQVTRAVSEVSAIKTAESAILEGKEIVSSATPKDQYDYGFTSTLLDGSQSOIY 94

QY 68 TNNKDGTVELVATLKGSSSAIKGAVITVSRKNDGVWNCITTKPTPAKPNYPANCPNS 127
 DB 95 TNNKDGTVELVATLKGSSSAIKGAVITVSRKNDGVWNCITTKPTPAKPNYPANCPNS 154

RESULT 4
 US-08-919-597-108

; Sequence 108, Application US/08919597
 ; Patent No. 6054265

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Pettey, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/919,597
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/470,896
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 154 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-919-597-108

Query Match 93.0%; Score 597; DB 3; Length 154;
Best Local Similarity 98.3%; Pred. No. 4.8e-60;
Matches 118; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 8 ARTQVTRAVSEVSAIKTAESAILEGKEIVSAPKPDYDIGFTSTLLDGSQIOV 67
DB 35 ARTQVTRAVSEVSAIKTAESAILEGKEIVSAPKPDYDIGFTSTLLDGSQIOV 94
OY 68 TDNKGTELVATLGKSSGSAIKGAVITVSRKNDGVNCKITKPTTANKPNYPANCPNS 127
DB 95 TDNKGTELVATLGKSSGSAIKGAVITVSRKNDGVNCKITKPTTANKPNYPANCPNS 154

RESULT 5
US-08-475-668A-108
Sequence 108, Application US/08475668A
Patent No. 6060065
GENERAL INFORMATION:
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Pettey, Stephen R.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,668A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 154 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-475-668A-108

Query Match 93.0%; Score 597; DB 3; Length 154;
Best Local Similarity 98.3%; Pred. No. 4.8e-60;
Matches 118; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 8 ARTQVTRAVSEVSAIKTAESAILEGKEIVSAPKPDYDIGFTSTLLDGSQIOV 67
DB 35 ARTQVTRAVSEVSAIKTAESAILEGKEIVSAPKPDYDIGFTSTLLDGSQIOV 94
OY 68 TDNKGTELVATLGKSSGSAIKGAVITVSRKNDGVNCKITKPTTANKPNYPANCPNS 127
DB 95 TDNKGTELVATLGKSSGSAIKGAVITVSRKNDGVNCKITKPTTANKPNYPANCPNS 154

RESULT 6
US-08-485-551A-108
Sequence 108, Application US/08485551A
Patent No. 6068973
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Pettey, Stephen R.
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485, 551A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-023
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 154 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-485-551A-108

Query Match 93.0%; Score 597; DB 3; Length 154;
Best Local Similarity 98.3%; Pred. No. 4.8e-60;
Matches 118; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 ARQVTVRAVSEVSALKTAEASALLEGKEIVSATPKDQYDIGFTSTLLDGSQIOY 67
DB 35 ARQVTVRAVSEVSALKTAEASALLEGKEIVSATPKDQYDIGFTSTLLDGSQIOY 94
QY 68 TDNKGTVELVATLKGSSGSAIKGAVITVSRKNDGVWNCCKITKPTAKPNYPANCPNS 127
DB 95 TDNKGTVELVATLKGSSGSAIKGAVITVSRKNDGVWNCCKITKPTAKPNYPANCPNS 154

RESULT 7

US-08-471-913A-108
Sequence 108, Application US/08471913A
Patent No. 6093794

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.
APPLICANT: Mathews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
NUMBER OF SEQUENCES: 214
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,913A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 154 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-471-913A-108

Query Match 93.0%; Score 597; DB 3; Length 154;
Best Local Similarity 98.3%; Pred. No. 4.8e-60;
Matches 118; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 ARQVTVRAVSEVSALKTAEASALLEGKEIVSATPKDQYDIGFTSTLLDGSQIOY 67
DB 35 ARQVTVRAVSEVSALKTAEASALLEGKEIVSATPKDQYDIGFTSTLLDGSQIOY 94
QY 68 TDNKGTVELVATLKGSSGSAIKGAVITVSRKNDGVWNCCKITKPTAKPNYPANCPNS 127
DB 95 TDNKGTVELVATLKGSSGSAIKGAVITVSRKNDGVWNCCKITKPTAKPNYPANCPNS 154

RESULT 8

US-08-485-264A-108
Sequence 108, Application US/08485264A
Patent No. 6228983

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.
APPLICANT: Mathews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING
NUMBER OF SEQUENCES: 232
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,264A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-021
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 154 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-485-264A-108

APPLICATION NUMBER: US/07/927,797
FILING DATE: 10-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 344,565
FILING DATE: 28-APR-1989
SEQ ID NO: 7
LENGTH: 19
5445818-7

Query Match 17.9%; Score 115; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.3e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 106 CKITKPTAMKPNYPANPC 124
DB 1 CKITKPTAMKPNYPANPC 19

RESULT 12
US-07-638-492-10
Sequence 10, Application US/07638492
Patent No. 5494672
GENERAL INFORMATION:
APPLICANT: Hodges, Robert S.
APPLICANT: Paranchych, William
APPLICANT: Irvin, Randall T.
APPLICANT: Lee, Kok K.
APPLICANT: Parimi, Satry A.
APPLICANT: Zoutman, Dick E.
APPLICANT: Doly, Peter C.
APPLICANT: Wong, Wah Y.
TITLE OF INVENTION: Pseudomonas Peptide Composition and
TITLE OF INVENTION: Method
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/638,492
FILING DATE: 04-JAN-1991
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8900-0002.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: peptide 10
US-07-638-492-10

Query Match 15.3%; Score 98; DB 1; Length 23;

Best Local Similarity 68.2%; Pred. No. 8e-05;
Matches 15; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
QY 106 CKITKPTAMKPNYPANPCNS 127
DB 2 CSISTPTAMKPNYPANPCNS 23

RESULT 13
US-07-638-492-8
Sequence 8, Application US/07638492
Patent No. 5494672
GENERAL INFORMATION:
APPLICANT: Hodges, Robert S.
APPLICANT: Paranchych, William
APPLICANT: Irvin, Randall T.
APPLICANT: Lee, Kok K.
APPLICANT: Parimi, Satry A.
APPLICANT: Zoutman, Dick E.
APPLICANT: Doly, Peter C.
APPLICANT: Wong, Wah Y.
TITLE OF INVENTION: Pseudomonas Peptide Composition and
TITLE OF INVENTION: Method
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/638,492
FILING DATE: 04-JAN-1991
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8900-0002.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: peptide 8
US-07-638-492-8

Query Match 14.6%; Score 94; DB 1; Length 23;
Best Local Similarity 72.7%; Pred. No. 0.00023;
Matches 16; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 106 CKITKPTAMKPNYPANPCNS 127
DB 2 CSISTPTAMKPNYPANPCNS 23

RESULT 14
US-07-638-492-9
Sequence 9, Application US/07638492

```

: Patent No. 5494672
:
: GENERAL INFORMATION:
: APPLICANT: Hodges, Robert S.
: APPLICANT: Paranchych, William
: APPLICANT: Irvin, Randall T.
: APPLICANT: Lee, Kok K.
: APPLICANT: Parimi, Sastry A.
: APPLICANT: Zoutman, Dick E.
: APPLICANT: Doig, Peter C.
: APPLICANT: Wong, Mah Y.
: TITLE OF INVENTION: Pseudomonas Peptide Composition and
: TITLE OF INVENTION: Method
: NUMBER OF SEQUENCES: 15
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Dehlinger & Associates
: STREET: 350 Cambridge Avenue, Suite 250
: CITY: Palo Alto
: STATE: CA
: COUNTRY: USA
: ZIP: 94306
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/638,492
: FILING DATE: 04-JAN-1991
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: Sholtz, Charles K.
: REGISTRATION NUMBER: 38,615
: REFERENCE/DOCKET NUMBER: 8900-0002.21
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 324-0880
: TELEFAX: (415) 324-0960
: INFORMATION FOR SEQ. ID NO.: 9:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 23 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: HYPOTHEICAL: NO
: ANTI-SENSE: NO
: ORIGINAL SOURCE:
: INDIVIDUAL ISOLATE: peptide 9
:
: US-07-638-492-9
:
: Query Match 14.6%; Score 94; DB 1; Length 23;
: Best Local Similarity 72.7%; Pred. No. 0.00023;
: Matches 16; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
:
: QY 106 CKIKPTAMKPNYPANCPNS 127
: Db 2 CGITGSEPTMKNTYRANCPKS 23
:
: RESULT 15
: US-08-084-739-12
: Sequence 12, Application US/08084739
: Patent No. 5468484
:
: GENERAL INFORMATION:
: APPLICANT: Hodges, Robert S.
: APPLICANT: Irvin, Randall T.
: APPLICANT: Paranchych, William
: APPLICANT: Sokol, Pamela A.
: APPLICANT: Woods, Donald E.
: TITLE OF INVENTION: Pseudomonas Exoenzyme S Peptide
: TITLE OF INVENTION: Composition and Method
: NUMBER OF SEQUENCES: 12
: CORRESPONDENCE ADDRESS:

```

ADDRESSEE: Law Offices of Peter Dellinger
STREET: 350 Cambridge Avenue, Suite 300
City: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Version #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/084,739
FILING DATE: 28-JUN-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/721,759
FILING DATE: 25-JUN-1991

ATTORNEY/AGENT INFORMATION:
NAME: Fadian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8900-0004.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960

INFORMATION FOR SEQ. ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
TOPOLOGY: both
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: 492c, Fig. 8

US-08-084-739-12

Query March	14.0%	Score 90:	DB 1:	Length 22:
Best Local Similarity	75.0%	Pred. No. 0.0006:		
Matches 15: Conservative	1:	Mismatches 4:	Indels 0:	Gaps 0:
OY	106	CKITKTPAMKPNTPANCP	125	
ibb	2	CGITGSPITNKANYANPANC	21	

Search completed: February 8, 2002, 15:25:12
Job time: 117 sec

Fri Feb 8 15:44:55 2002

us-09-865-159-8.ra1

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd

OM protein - protein search, using sw model

Run on: February 8, 2002, 15:32:39 ; Search time 353.09 Seconds
(without alignments)
99.868 Million cell updates/sec

Title:	US-09-865-159-8
Perfect score:	642
Sequence:	1 ALEGTFAQTQVTRAVSEVS.....ITKPTAMKKNYAPANCPS 127

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

```
Searched:      3148936 seqs, 277657034 residues
Total number of hits satisfying chosen parameters:  3148936
```

```
Minimum DB seq length: 0
Maximum DB seq length: 20000000000
```

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

Pending_Patents_AA_Main:*

- 1: /cgn2_6/ptodata/2/paa/PCNUS.COMB.pep.*
- 2: /cgn2_6/ptodata/2/paa/US06.COMB.pep.*
- 3: /cgn2_6/ptodata/2/paa/US07.COMB.pep.*
- 4: /cgn2_6/ptodata/2/paa/US08.COMB.pep.*
- 5: /cgn2_6/ptodata/2/paa/US081.COMB.pep.*
- 6: /cgn2_6/ptodata/2/paa/US082.COMB.pep.*
- 7: /cgn2_6/ptodata/2/paa/US083.COMB.pep.*
- 8: /cgn2_6/ptodata/2/paa/US084.COMB.pep.*
- 9: /cgn2_6/ptodata/2/paa/US085.COMB.pep.*
- 10: /cgn2_6/ptodata/2/paa/US086.COMB.pep.*
- 11: /cgn2_6/ptodata/2/paa/US087.COMB.pep.*
- 12: /cgn2_6/ptodata/2/paa/US088.COMB.pep.*
- 13: /cgn2_6/ptodata/2/paa/US089.COMB.pep.*
- 14: /cgn2_6/ptodata/2/paa/US090.COMB.pep.*
- 15: /cgn2_6/ptodata/2/paa/US091.COMB.pep.*
- 16: /cgn2_6/ptodata/2/paa/US092.COMB.pep.*
- 17: /cgn2_6/ptodata/2/paa/US093.COMB.pep.*
- 18: /cgn2_6/ptodata/2/paa/US094.COMB.pep.*
- 19: /cgn2_6/ptodata/2/paa/US095.COMB.pep.*
- 20: /cgn2_6/ptodata/2/paa/US096.COMB.pep.*
- 21: /cgn2_6/ptodata/2/paa/US097.COMB.pep.*
- 22: /cgn2_6/ptodata/2/paa/US098.COMB.pep.*
- 23: /cgn2_6/ptodata/2/paa/US099.COMB.pep.*
- 24: /cgn2_6/ptodata/2/paa/US60.COMB.pep.*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB	ID	Description
1	642	100.0	127	17	US-09-329-884-8	Sequence 8, Appli
2	597	93.0	154	7	US-08-360-107-118	Sequence 118, App
3	597	93.0	154	8	US-08-470-896-108	Sequence 108, App
4	597	93.0	154	8	US-08-471-913-108	Sequence 108, App
5	597	93.0	154	8	US-08-474-349-108	Sequence 108, App
6	597	93.0	154	8	US-08-475-668-108	Sequence 108, App
7	597	93.0	154	8	US-08-475-668-108	Sequence 108, App
8	597	93.0	154	8	US-08-484-223-108	Sequence 108, App
9	597	93.0	154	8	US-08-484-223A-108	Sequence 108, App

10	597	93.0	154	8	US-08-485-56-108	Sequence 108, App
11	597	93.0	154	8	US-08-485-56-108	Sequence 108, App
12	597	93.0	154	8	US-08-485-56-108	Sequence 108, App
13	597	93.0	154	8	US-08-485-56-108	Sequence 108, App
14	597	93.0	154	8	US-08-485-56-108	Sequence 108, App
15	597	93.0	154	8	US-08-485-56-108	Sequence 108, App
16	597	93.0	154	8	US-08-485-56-108	Sequence 108, App
17	597	93.0	154	13	US-08-919-600-108	Sequence 108, App
18	597	93.0	154	19	US-09-502-445-108	Sequence 108, App
19	186.5	29.0	127	17	US-09-329-884-10	Sequence 10, App
20	137.5	21.4	122	17	US-09-329-884-6	Sequence 6, App
21	134	20.9	123	17	US-09-329-884-4	Sequence 4, App
22	119	18.5	168	17	US-09-329-884-22	Sequence 22, App
23	117.5	18.3	168	17	US-09-329-884-20	Sequence 20, App
24	115.5	18.0	169	17	US-09-329-884-14	Sequence 14, App
25	115	17.9	19	17	US-09-306-241-12	Sequence 12, App
26	115	17.9	19	17	US-09-345-624-11	Sequence 12, App
27	115	17.9	19	17	US-09-345-624-12	Sequence 12, App
28	114	17.8	169	17	US-09-328-352-6277	Sequence 6277, App
29	114	17.8	169	17	US-09-329-884-12	Sequence 12, App
30	112.5	17.5	139	22	US-09-848-616-140	Sequence 140, App
31	101.5	15.8	129	17	US-09-329-884-2	Sequence 2, App
32	98	15.3	17	9	US-08-576-97-48	Sequence 4, App
33	98	15.3	17	17	US-09-337-993-4	Sequence 4, App
34	87	13.6	19	17	US-09-306-241-14	Sequence 14, App
35	87	13.6	19	17	US-09-345-624-11	Sequence 14, App
36	87	13.6	19	17	US-09-345-624-14	Sequence 14, App
37	84	13.1	82	3	US-07-803-762A-19	Sequence 19, App
38	84	13.1	84	3	US-07-809-762A-19	Sequence 19, App
39	83	12.9	19	17	US-09-306-241-13	Sequence 13, App
40	83	12.9	19	17	US-09-345-624-13	Sequence 13, App
41	83	12.9	19	17	US-09-345-624-13	Sequence 13, App
42	83	12.9	153	19	US-09-540-236-6689	Sequence 3689, App
43	83	12.9	153	24	US-60-128-476-4820	Sequence 4820, App
44	83	12.9	175	17	US-09-329-884-18	Sequence 18, App
45	81.5	12.7	175	17	US-09-329-884-16	Sequence 16, App

ALIGNMENTS

```

1 RESULT
2 US-09-329-884-8
3 Sequence 8, Application US/09329884
4 GENERAL INFORMATION:
5
6 APPLICANT: Irvin, Randall T.
7 APPLICANT: Hodges, Robert S.
8
9 TITLE OF INVENTION: PSEUDOMONAS TREATMENT
10 TITLE OF INVENTION: COMPOSITION AND METHOD
11 FILE REFERENCE: 8900-0008, 30
12 CURRENT APPLICATION NUMBER: US/09/329, 884
13 CURRENT FILING DATE: 1999-06-11
14 EARLIER APPLICATION NUMBER: US 60/089,155
15 EARLIER FILING DATE: 1998-06-12
16 NUMBER OF SEQ ID NOS: 22
17 SOFTWARE: FastSeq for Windows Version 3.0
18 SEQ ID NO: 8
19 LENGTH: 127
20 TYPE: PRT
21 ORGANISM: Pseudomonas aeruginosa
22 US-09-329-884-8

```

Query Match	100.0%;	Score 642;	DB 17;	Length 127;
Best Local Similarity	100.0%;	Pred. No. 7.4e-61;		
Matches 127;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 ALEGEFAROVTVRAVSEVSAIKTAAEALIEGKEIYVSAPPKTOYDIGTETSLDGS 60
1 ALEGEFAROVTVRAVSEVSAIKTAAEALIEGKEIYVSAPPKTOYDIGTETSLDGS 60
1 ALEGEFAROVTVRAVSEVSAIKTAAEALIEGKEIYVSAPPKTOYDIGTETSLDGS 60
1 ALEGEFAROVTVRAVSEVSAIKTAAEALIEGKEIYVSAPPKTOYDIGTETSLDGS 60
QY 61 GKSOIQVNDKNGVVELATLIGKSSGSAIKGAVITVSRKNDGVNCKITPTPAKRPNYA 120
1 GKSOIQVNDKNGVVELATLIGKSSGSAIKGAVITVSRKNDGVNCKITPTPAKRPNYA 120
1 GKSOIQVNDKNGVVELATLIGKSSGSAIKGAVITVSRKNDGVNCKITPTPAKRPNYA 120
1 GKSOIQVNDKNGVVELATLIGKSSGSAIKGAVITVSRKNDGVNCKITPTPAKRPNYA 120

Db 61 GKSQIQTVDNKGTVELVATLGGSSGSAIKGAVITVSRKNDGVNCKITTKPTAMKPNTYA 120
QY 121 PANCNS 127
Db 121 PANCNS 127

RESULT 2

US-08-360-107-118

Sequence 118, Application US/08360107
GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 137
CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,107
FILING DATE: 20-DEC-1994
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 118:

SEQUENCE CHARACTERISTICS:
LENGTH: 154 amino acids
TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-08-360-107-118

Query Match 93.0%; Score 597; DB 7; Length 154;
Best Local Similarity 98.3%; Pred. NO. 6.9e-56;
Matches 118; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 ARTQVTRAVSEVSAIKTAESAILEGKEIVSSATPKDYDIDGFTSTLLDGGSGKSOIQY 67
Db 35 ARTQVTRAVSEVSAIKTAESAILEGKEIVSSATPKDYDIDGFTSTLLDGGSGKSOIQY 94
QY 68 TDNKGTVELVATLGGSSGSAIKGAVITVSRKNDGVNCKITTKPTAMKPNTYAPANCPS 127
Db 95 TDNKGTVELVATLGGSSGSAIKGAVITVSRKNDGVNCKITTKPTAMKPNTYAPANCPS 154

RESULT 3

US-08-470-896-108

Sequence 108, Application US/08470896
GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,896
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 108:

SEQUENCE CHARACTERISTICS:
LENGTH: 154 amino acids
TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-08-470-896-108

Query Match 93.0%; Score 597; DB 8; Length 154;
Best Local Similarity 98.3%; Pred. NO. 6.9e-56;
Matches 118; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 ARTQVTRAVSEVSAIKTAESAILEGKEIVSSATPKDYDIDGFTSTLLDGGSGKSOIQY 67
Db 35 ARTQVTRAVSEVSAIKTAESAILEGKEIVSSATPKDYDIDGFTSTLLDGGSGKSOIQY 94
QY 68 TDNKGTVELVATLGGSSGSAIKGAVITVSRKNDGVNCKITTKPTAMKPNTYAPANCPS 127
Db 95 TDNKGTVELVATLGGSSGSAIKGAVITVSRKNDGVNCKITTKPTAMKPNTYAPANCPS 154

RESULT 4

US-08-471-913-108

Sequence 108, Application US/08471913
GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE
FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 209

RESULT 6
US-08-474-349A-108
Sequence 108, Application US/08474349A
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Peteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 517
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,349A
FILING DATE: 07-JUN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-024
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 154 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-474-349A-108

Query Match 93.0%; Score 597; DB 8; Length 154;
Best Local Similarity 98.3%; Pred. No. 6.9e-56;
Matches 118; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 ARTQVTRAVSEVSALKTAAESALIEGKEIYSSATPKDTQYDIGFTSTLLDGSQIOY 67
DB 35 ARTQVTRAVSEVSALKTAAESALIEGKEIYSSATPKDTQYDIGFTSTLLDGSQIOY 94
QY 68 TDNKGTVELVATLGKSSGSAIKGAVITVSRKNDGVNCKITKTPAMKPNYAPANCPNS 127
DB 95 TDNKGTVELVATLGKSSGSAIKGAVITVSRKNDGVNCKITKTPAMKPNYAPANCPNS 154

RESULT 7

US-08-475-668-108
Sequence 108, Application US/08475668

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,668
FILING DATE: 07-JUN-1995

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-026
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864

INFORMATION FOR SEQ ID NO: 108:

SEQUENCE CHARACTERISTICS:
LENGTH: 154 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-475-668-108

Query Match 93.0%; Score 597; DB 8; Length 154;
Best Local Similarity 98.3%; Pred. No. 6.9e-56;
Matches 118; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 ARTQVTRAVSEVSALKTAAESALIEGKEIYSSATPKDTQYDIGFTSTLLDGSQIOY 67
DB 35 ARTQVTRAVSEVSALKTAAESALIEGKEIYSSATPKDTQYDIGFTSTLLDGSQIOY 94
QY 68 TDNKGTVELVATLGKSSGSAIKGAVITVSRKNDGVNCKITKTPAMKPNYAPANCPNS 127
DB 95 TDNKGTVELVATLGKSSGSAIKGAVITVSRKNDGVNCKITKTPAMKPNYAPANCPNS 154

RESULT 8

US-08-484-223-108
Sequence 108, Application US/08484223

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223
FILING DATE: 07-JUN-1995

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864

INFORMATION FOR SEQ ID NO: 108:

SEQUENCE CHARACTERISTICS:
LENGTH: 154 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-484-223-108

Query Match 93.0%; Score 597; DB 8; Length 154;
Best Local Similarity 98.3%; Pred. No. 6.9e-56;
Matches 118; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 ARTQVTRAVSEVSALKTAAESALIEGKEIYSSATPKDTQYDIGFTSTLLDGSQIOY 67
DB 35 ARTQVTRAVSEVSALKTAAESALIEGKEIYSSATPKDTQYDIGFTSTLLDGSQIOY 94
QY 68 TDNKGTVELVATLGKSSGSAIKGAVITVSRKNDGVNCKITKTPAMKPNYAPANCPNS 127
DB 95 TDNKGTVELVATLGKSSGSAIKGAVITVSRKNDGVNCKITKTPAMKPNYAPANCPNS 154

Db 95 TDNDGTVELVATLGKSSGSAIKGAVITVSRKNDGVNMCKITKTPTAMPNYPANCPKS 154

RESULT 9

US-08-484-223A-108
Sequence 108, Application US/08484223A

GENERAL INFORMATION:

APPLICANT: Bolognesi, Daniel P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Pelletway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 108:

SEQUENCE CHARACTERISTICS:
LENGTH: 154 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-484-223A-108

Query Match 93.0%; Score 597; DB 8; Length 154;
Best Local Similarity 98.3%; Pred. No. 6.9e-56;
Matches 118; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 ARTQYTRAVSEYSAIKTAESAILEGKEIVSATPKDYDIGFTSTLLDSSGSKSQIOY 67
DB 35 ARTQYTRAVSEYSAIKTAESAILEGKEIVSATPKDYDIGFTSTLLDSSGSKSQIOY 94
QY 68 TDNDGTVELVATLGKSSGSAIKGAVITVSRKNDGVNMCKITKTPTAMPNYPANCPNS 127
DB 95 TDNDGTVELVATLGKSSGSAIKGAVITVSRKNDGVNMCKITKTPTAMPNYPANCPKS 154

RESULT 10

US-08-485-546-108
Sequence 108, Application US/08485546

GENERAL INFORMATION:

APPLICANT: Bolognesi, Daniel P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.
APPLICANT: Pelletway, Stephen R.
APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,546
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-028
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 108:

SEQUENCE CHARACTERISTICS:
LENGTH: 154 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-485-546-108

Query Match 93.0%; Score 597; DB 8; Length 154;
Best Local Similarity 98.3%; Pred. No. 6.9e-56;
Matches 118; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 ARTQYTRAVSEYSAIKTAESAILEGKEIVSATPKDYDIGFTSTLLDSSGSKSQIOY 67
DB 35 ARTQYTRAVSEYSAIKTAESAILEGKEIVSATPKDYDIGFTSTLLDSSGSKSQIOY 94
QY 68 TDNDGTVELVATLGKSSGSAIKGAVITVSRKNDGVNMCKITKTPTAMPNYPANCPNS 127
DB 95 TDNDGTVELVATLGKSSGSAIKGAVITVSRKNDGVNMCKITKTPTAMPNYPANCPKS 154

RESULT 11

US-08-485-546A-108
Sequence 108, Application US/08485546A

GENERAL INFORMATION:

APPLICANT: Bolognesi, Daniel P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Pelletway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 214
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York

STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,546A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-028
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 154 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-485-546A-108

Query Match 93.0%; Score 597; DB 8; Length 154;
Best Local Similarity 98.3%; Pred. No. 6.9e-56;
Matches 118; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 ARTQYTRAVSEYSAIKTAESAILEGKEIVSATPKDYDYGFTSTLLDGSQIOY 67
DB 35 ARTQYTRAVSEYSAIKTAESAILEGKEIVSATPKDYDYGFTSTLLDGSQIOY 94

QY 68 TDNKDGTVELVATLTKSSGSAIKGAVITVSRKNDGVWNCIKTKPTAKPNYPANPCPS 127
DB 95 TDNDGTVELVATLTKSSGSAIKGAVITVSRKNDGVWNCIKTKPTAKPNYPANPCPS 154

RESULT 12
US-08-485-551-108
Sequence 108, Application US/08485551
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,551
FILING DATE: 07-JUN-1995

CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-023
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 154 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-485-551-108

Query Match 93.0%; Score 597; DB 8; Length 154;
Best Local Similarity 98.3%; Pred. No. 6.9e-56;
Matches 118; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 ARTQYTRAVSEYSAIKTAESAILEGKEIVSATPKDYDYGFTSTLLDGSQIOY 67
DB 35 ARTQYTRAVSEYSAIKTAESAILEGKEIVSATPKDYDYGFTSTLLDGSQIOY 94

QY 68 TDNKDGTVELVATLTKSSGSAIKGAVITVSRKNDGVWNCIKTKPTAKPNYPANPCPS 127
DB 95 TDNDGTVELVATLTKSSGSAIKGAVITVSRKNDGVWNCIKTKPTAKPNYPANPCPS 154

RESULT 13
US-08-487-266-108
Sequence 108, Application US/08487266
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,266
FILING DATE: 07-JUN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-025
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 154 amino acids

TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-487-266-108

Query Match 93.0%; Score 597; DB 8; Length 154;
Best Local Similarity 98.3%; Pred. No. 6.9e-56;
Matches 118; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 8 ARTQVTRAVSEVSALKTAESAILEGKEIVSSATPKDYDIGFTSTLLDGSQIOY 67
DB 35 ARTQVTRAVSEVSALKTAESAILEGKEIVSSATPKDYDIGFTSTLLDGSQIOY 94
OY 68 TDNKGTVELVATLGKSSGSAIKGAVITVSRKNDGVWCKITKPTANKPNYAPANCPS 127
DB 95 TDNKGTVELVATLGKSSGSAIKGAVITVSRKNDGVWCKITKPTANKPNYAPANCPS 154

RESULT 14

US-08-487-266A-108
Sequence 108, Application US/08487266A
GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Peteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION
NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,266A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-025
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:

LENGTH: 154 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-487-266A-108

Query Match 93.0%; Score 597; DB 8; Length 154;
Best Local Similarity 98.3%; Pred. No. 6.9e-56;
Matches 118; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 8 ARTQVTRAVSEVSALKTAESAILEGKEIVSSATPKDYDIGFTSTLLDGSQIOY 67

DB 35 ARTQVTRAVSEVSALKTAESAILEGKEIVSSATPKDYDIGFTSTLLDGSQIOY 94
OY 68 TDNKGTVELVATLGKSSGSAIKGAVITVSRKNDGVWCKITKPTANKPNYAPANCPS 127
DB 95 TDNKGTVELVATLGKSSGSAIKGAVITVSRKNDGVWCKITKPTANKPNYAPANCPS 154

RESULT 15

US-08-487-355-108
Sequence 108, Application US/08487355
GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Peteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS B VIRUS
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,355
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-027
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:

LENGTH: 154 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-487-355-108

Query Match 93.0%; Score 597; DB 8; Length 154;
Best Local Similarity 98.3%; Pred. No. 6.9e-56;
Matches 118; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 8 ARTQVTRAVSEVSALKTAESAILEGKEIVSSATPKDYDIGFTSTLLDGSQIOY 67
DB 35 ARTQVTRAVSEVSALKTAESAILEGKEIVSSATPKDYDIGFTSTLLDGSQIOY 94
OY 68 TDNKGTVELVATLGKSSGSAIKGAVITVSRKNDGVWCKITKPTANKPNYAPANCPS 127
DB 95 TDNKGTVELVATLGKSSGSAIKGAVITVSRKNDGVWCKITKPTANKPNYAPANCPS 154

Search completed: February 8, 2002, 15:32:39
Job time: 564 sec

Fri Feb 8 15:44:55 2002

us-09-865-159-8.rapm

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 8, 2002, 15:26:38 ; Search time 37.1 Seconds

(without alignments)
152.410 Million cell updates/sec

Title: US-09-865-159-8

Sequence: 1 ALEGEFARTQVTRAVSEVS.....ITKPTAKMPNTPANCNS 127

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 211743 seqs, 44522877 residues

Total number of hits satisfying chosen parameters: 211743

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 08
Maximum Match 1008

Listing first 45 summaries

Database :

Pending Patents, AA, New: *
1: /cgn2_6/prodata/2/paa/PCT_NEW_COMB.pep: *
2: /cgn2_6/prodata/2/paa/US06_NEW_COMB.pep: *
3: /cgn2_6/prodata/2/paa/US07_NEW_COMB.pep: *
4: /cgn2_6/prodata/2/paa/US08_NEW_COMB.pep: *
5: /cgn2_6/prodata/2/paa/US09_NEW_COMB.pep: *
6: /cgn2_6/prodata/2/paa/US10_NEW_COMB.pep: *
7: /cgn2_6/prodata/2/paa/US60_NEW_COMB.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	642	100.0	127	5	US-09-865-159-8
2	186.5	29.0	127	5	US-09-865-159-10
3	137.5	21.4	122	5	US-09-865-159-6
4	134	20.9	123	5	US-09-865-159-4
5	119	18.5	128	5	US-09-865-159-22
6	117.5	18.3	168	5	US-09-865-159-20
7	115.5	18.0	169	5	US-09-865-159-14
8	114	17.8	169	5	US-09-865-159-12
9	101.5	15.9	129	5	US-09-865-159-2
10	83	12.9	175	5	US-09-865-159-18
11	81.5	12.7	175	5	US-09-865-159-16
12	79	12.3	934	5	US-09-696-1888-19
13	75	11.7	581	5	US-09-999-201-3
14	75	11.7	857	5	US-09-708-427-4849
15	75	11.7	931	5	US-09-708-427-4848
16	75	11.7	1076	5	US-09-708-427-4847
17	74.5	11.6	1240	6	US-10-032-585-7319
18	72.5	11.3	742	6	US-10-015-127-10181
19	72	11.2	226	5	US-09-708-427-50429
20	70.5	11.0	286	5	US-09-708-427-15689
21	70.5	11.0	328	5	US-09-708-427-15688
22	70.5	11.0	392	5	US-09-708-427-15687
23	70.5	11.0	581	6	US-10-015-127-10008
24	70.5	11.0	662	5	US-09-708-427-12261
25	70.5	11.0	685	5	US-09-708-427-12260
26	70.5	11.0	718	5	US-09-708-427-12259

27	70.5	11.0	870	5	US-09-605-7038-1686	Sequence 1686, Ap
28	70.5	11.0	1270	5	US-09-708-427-27601	Sequence 27601, A
29	70.5	11.0	1462	5	US-09-708-427-27600	Sequence 27600, A
30	70.5	11.0	1480	5	US-09-708-427-27599	Sequence 27599, A
31	70	10.9	2434	5	US-09-815-242-5835	Sequence 5835, Ap
32	70	10.9	5795	5	US-09-815-242-12610	Sequence 12610, A
33	70	10.9	6281	5	US-09-815-242-12996	Sequence 12996, A
34	69.5	10.8	613	5	US-09-708-427-1917	Sequence 1917, Ap
35	69.5	10.8	614	5	US-09-708-427-1916	Sequence 1916, Ap
36	69	10.7	298	5	US-09-708-427-8492	Sequence 8492, Ap
37	69	10.7	441	5	US-09-708-427-8491	Sequence 8491, Ap
38	68	10.6	164	5	US-09-675-784A-13581	Sequence 13581, A
39	68	10.6	403	5	US-09-620-394B-6539	Sequence 6539, Ap
40	68	10.6	403	5	US-09-708-427-22106	Sequence 22106, A
41	68	10.6	436	5	US-09-620-394B-6538	Sequence 6538, Ap
42	68	10.6	436	5	US-09-708-427-22105	Sequence 22105, A
43	68	10.6	508	5	US-09-620-394B-6537	Sequence 6537, Ap
44	68	10.6	508	5	US-09-708-427-22104	Sequence 22104, A
45	68	10.6	722	5	US-09-815-242-13748	Sequence 13748, A

ALIGNMENTS

```
RESULT 1
US-09-865-159-8
: Sequence 8, Application US/09865159
: GENERAL INFORMATION:
: APPLICANT: Irvlin, Randall T.
: TITLE OF INVENTION: PSEUDOMONAS TREATMENT
: FILE REFERENCE: 8900-0008.30
: CURRENT APPLICATION NUMBER: US/09/865,159
: PRIOR FILING DATE: 2001-05-24
: PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329,884
: PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
: NUMBER OF SEQ ID NOS: 22
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 8
: LENGTH: 127
: TYPE: PR1
: ORGANISM: Pseudomonas aeruginosa
US-09-865-159-8

Query Match      100.0%; Score 642; DB 5; Length 127;
Best Local Similarity 100.0%; Pred. No. 7e-53;
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ALEGEFARTQVTRAVSEVSALKTAESAIIIEGKEIVSAPPKDYDIDGFTSTLLDGS 60
|||||
Db 1 ALEGEFARTQVTRAVSEVSALKTAESAIIIEGKEIVSAPPKDYDIDGFTSTLLDGS 60

OY 61 GKSQIQVNDKDGVEIVATLGKSSGSAIKGAVITVSRKNCVNMCKITKPTAKPNYA 120
|||||
Db 61 GKSQIQVNDKDGVEIVATLGKSSGSAIKGAVITVSRKNCVNMCKITKPTAKPNYA 120

OY 121 PANCNPS 127
|||||
Db 121 PANCNPS 127

RESULT 2
US-09-865-159-10
: Sequence 10, Application US/09865159
: GENERAL INFORMATION:
: APPLICANT: Irvlin, Randall T.
: TITLE OF INVENTION: PSEUDOMONAS TREATMENT
: FILE REFERENCE: 8900-0008.30
: CURRENT APPLICATION NUMBER: US/09/865,159
```

CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329,884
PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 127
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-865-159-10

Query Match
Best Local Similarity 29.0%; Score 186.5; DB 5; Length 127;
Matches 45; Conservative 25; Mismatches 44; Indels 13; Gaps 3;

QY 1 ALEGEFARTQVTRAVSEVSAKTAESAILGKEIYSSATPKDTQYDIGTFESTLIDGS 60
DB 1 ALEGEFARSQVSRVMAEAGSLKTAVEACIADGRTAVGTAA--GQCDPGATGSSLLTGA 57
QY 61 GKSQ-----IQVDNKGIVELVATLGKSSGAIKGAVITVSRKNDGVNCKITKT 111
DB 58 SQTQLEPTNTGVPQVLDPLTTQTTIATFGNGASAIISQTLTWDVNGVMS-ATTV 116
QY 112 PTAKPN 118
DB 117 DAKFRPN 123

RESULT 3
US-09-865-159-6
Sequence 6, Application US/09865159
GENERAL INFORMATION:
APPLICANT: Irvn, Randall T.
TITLE OF INVENTION: PSEUDOMONAS TREATMENT
FILE REFERENCE: 8900-0008.30
CURRENT APPLICATION NUMBER: US/09/865,159
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329,884
PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 122
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-865-159-6

Query Match
Best Local Similarity 21.4%; Score 137.5; DB 5; Length 122;
Matches 42; Conservative 18; Mismatches 42; Indels 21; Gaps 5;

QY 1 ALEGEFARTQVTRAVSEVSAKTAESAILGKEIYSSATPKDTQYDIGTFESTLIDGS 58
DB 1 ALEGEFARSQVSRVMAEAGSLKTAVEACIADGRTAVGTAA--GQCDPGATGSSLLTGA 57
QY 59 -----GSGKSOIQVTDNKGIVELVATLGKSS-GSAIKGAVITVSRKNDGVNCKIT 109
DB 53 AGVEPDANKIGVAVNAIEDSGAGDITFTTGTGSSPKNATK--VITLNRADGVMAKCKSI 110
QY 110 KTRP 112
DB 111 QDP 113

RESULT 4
US-09-865-159-4
Sequence 4, Application US/09865159
GENERAL INFORMATION:
APPLICANT: Irvn, Randall T.

APPLICANT: Hodges, Robert S.
TITLE OF INVENTION: PSEUDOMONAS TREATMENT
FILE REFERENCE: 8900-0008.30
CURRENT APPLICATION NUMBER: US/09/865,159
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329,884
PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 123
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-865-159-4

Query Match
Best Local Similarity 20.9%; Score 134; DB 5; Length 123;
Matches 40; Conservative 19; Mismatches 41; Indels 14; Gaps 6;

QY 1 ALEGEFARTQVTRAVSEVSAKTAESAILGKEIYSSATPKDTQYDIGTFESTLIDGS 55
DB 1 ALEGEFARSQVSRVMAEAGSLKTAVEACIADGRTAVGTAA--GQCDPGATGSSLLTGA 57
QY 56 LIDGSGKSOIQVTDNKGIVELVATLGKSSGAIKGAVITVSRKNDGVNCKITKT 106
DB 61 L-----GTIAK-PDPADGTADITLFTTNG-GAGFRNKGKILTRTADGIMKC 108

RESULT 5
US-09-865-159-22
Sequence 22, Application US/09865159
GENERAL INFORMATION:
APPLICANT: Irvn, Randall T.
TITLE OF INVENTION: PSEUDOMONAS TREATMENT
FILE REFERENCE: 8900-0008.30
CURRENT APPLICATION NUMBER: US/09/865,159
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329,884
PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 22
LENGTH: 168
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-865-159-22

Query Match
Best Local Similarity 18.5%; Score 119; DB 5; Length 168;
Matches 41; Conservative 18; Mismatches 43; Indels 24; Gaps 6;

QY 1 ALEGEFARTQVTRAVSEVSAKTAESAILGKEIYSSATPKDTQYDIGTFESTLIDGS 57
DB 44 ALEKGGGGFARSQVSRVMAEAGSLKTAVEACIADGRTAVGTAA--GQCDPGATGSSLLTGA 57
QY 58 D-----GSGKSOIQVTDNKGIVELVATLGKSS-GSAIKGAVITVSRKNDGVNCKIT 106
DB 96 ETYAGVEPDANKIGVAVNAIEDSGAGDITFTTGTGSSPKNATK--VITLNRADGVMAKCKSI 110
QY 107 KTRP 112
DB 154 KSTDDP 159

RESULT 6
US-09-865-159-20
Sequence 20, Application US/09865159
GENERAL INFORMATION:

```

: APPLICANT: Irvin, Randall T.
: APPLICANT: Hodges, Robert S.
: TITLE OF INVENTION: PSEUDOMONAS TREATMENT
: TITLE OF INVENTION: COMPOSITION AND METHOD
: FILE REFERENCE: 8900-0008.30
: CURRENT APPLICATION NUMBER: US/09/865,159
: CURRENT FILING DATE: 2001-05-24
: PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329,884
: PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
: NUMBER OF SEQ ID NOS: 22
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 20
: LENGTH: 168
: TYPE: PRF
: ORGANISM: Pseudomonas aeruginosa
: US-09-865-159--20

```

Query Match	18.3%;	Score 117.5;	DB 5;	Length 168;
Best Local Similarity	31.7%;	Pred. No. 0.00072;		
Matches 38; Conservative	18;	Mismatches 43;	Indels 21;	Gaps 5;

```

QY 4 GTEFAHQVTVANSEVVALKTAALASALLEGEIYSSAKPKDQVDFIETSTLLD ---- 58
    | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 50 GCEPARSEGASALATINPLKTYVESLSRG - IAGS ----- KIKITTASTATEYAGV 100
QY 59 -----GSGKSIQVTVDMKDGVELVALLKSS -GSAIKGAVIYYSRKNDGYMNCITKTP 112
    | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 102 EPDANKIGVAVALEDSGAGIITTFQGTSSPANKAK -VITLNRPADGVACKSRQDP 150
    | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

```

```

RESULT 7
US-09-865-159-14
Sequence 14, Application US/09865159
GENERAL INFORMATION:
APPLICANT: Irvin, Randall T.
APPLICANT: Hodges, Robert S.
TITLE OF INVENTION: PSEUDOMONAS TREATMENT
FILE REFERENCE: 8900-0008.30
CURRENT APPLICATION NUMBER: US/09/865,159
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329,884
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 14
LENGTH: 169
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-865-159-14

```

Query Match	18.0%;	Score 115.57;	DB 5;	length 169;
Best Local Similarity	33.3%;	Pred. No. 0.0011;		
Matches	39;	Conservative 19;	Mismatches 42;	Indels 17; Gaps 7

OY	1	ALE---	GREFPRTQTRAVSEVSAKTAESAILEGKEIVS-----	SAMPKQNYDIGT	52
Db	44	ALEGGGGEPFARSEBASALASVNP	KLTYVEELISKWSVKSGETGTDATKKEVPEPLCAAD		103
OY	53	ESTLLDSSGKSOIQVTDNKDGT--	VELYATLGKSSGSAIKAVIYSR-KNDGWNVC		106
Db	104	ANKL---GTLALK-PDPADGTA	DTITLTFTTWG-GAGPKNKGGIITLITRAADGIMVC		154

RESULT 8
US-09-865-159-12
Sequence 12, Application US/09865159
GENERAL INFORMATION:
: APPLICANT: Irvlin, Randall T.
: APPLICANT: Hodges, Robert S.
: TITLE OF INVENTION: PSEUDOMONAS TREATMENT

TITLE: INVENTION: COMPOSITION AND METHOD
 FILE REFERENCE: 8900-0008.30
 CURRENT APPLICATION NUMBER: US/09/865,159
 CURRENT FILING DATE: 2001-05-24
 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329,884
 PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
 NUMBER OF SEQ. ID NOS: 22
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ. ID NO. 12
 LENGTH: 169
 TYPE: PR1
 ORGANISM: *Pseudomonas aeruginosa*
 US-09-865-159-12

2	Query Match	17.8%	Score 114	DE 5	length 169
3	Best Local Similarity	32.4%	Pred. No.	0.0015	
4	Matches	36	Conservative	19	Mismatches 42; Indels 14; Gaps 6

[illegible]

```

1 RESULT          9
2 US-09-865-159-2
3 : Sequence 2, Application US/09865159
4 : GENERAL INFORMATION:
5 :
6 : APPLICANT: Irvin, Randall T.
7 :
8 : TITLE OF INVENTION: PSEUDOMONAS TREATMENT
9 :
10 : FILE OF INVENTION: COMPOSITION AND METHOD
11 :
12 : FILE REFERENCE: 8900-0008.30
13 :
14 : CURRENT APPLICATION NUMBER: US/09/865,159
15 :
16 : PRIOR FILING DATE: 2001-05-24
17 :
18 : PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329,884
19 :
20 : PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
21 :
22 : NUMBER OF SEQ ID NOS: 22
23 :
24 : SOFTWARE: FASTSEQ for Windows Version 3.0.
25 :
26 : SEQ ID NO 2
27 :
28 : LENGTH: 129
29 :
30 : TYPE: FRT
31 :
32 : ORGANISM: Pseudomonas aeruginosa
33 :
34 : US-09-865-159-2

```

```

Query Match      15.8%: Score 101.5; DB 5; Length 129;
Best Local Similarity 28.6%: Pred. No. 0.016;
Matches 38; Conservative 18; Mismatches 56; Indels 21; Gaps 7

QY      1 ALEGEFAPRTQVTRAVSEVSAALTKTAESAALTEGKEIVSSATPKRDYDIDGTFESTLLDGS 60
      ||||| ||||| : : : |||
Db      1 ALEGEFAPRAOLSEEMTLASGLTKRVSDIFSQ-----DQSCPANTAAATGIERKT--DIN 53
      ||||| ||||| : : : |||

QY      61 GKSOIQVTDN---KDGVEIVLAVTLGKSS-GSAIKGAVITV---SRKNDGVANCKITPK 111
      || :|| :||| : :||| : :||| :
Db      54 GKYYAKVVTGGTAAASGCGTIVATMKASDVATPLRGKTLTLTLGNADKGSYTMAC---T 109
      || :|| :||| : :||| : :||| :

QY      112 PTAKKPNYAPANC 124
Db      110 SNA-DNKKYLPKTC 121
      || :|| :||| : :||| : :||| :

```

RESULT 10
US-09-865-159-18
; Sequence 18, Application US/09865155
; GENERAL INFORMATION:
; APPLICANT: Irvin, Randall T.
; APPLICANT: Hodges, Robert S.

;; TITLE OF INVENTION: PSEUDOMONAS TREATMENT
;; FILE OF INVENTION: COMPOSITION AND METHOD
;; FILE REFERENCE: 8900-0008.30
;; CURRENT APPLICATION NUMBER: US/09/865,159
;; CURRENT FILING DATE: 2001-05-24
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329,884
;; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
;; NUMBER OF SEQ ID NOS: 22
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 18
;; LENGTH: 175
;; TYPE: PR1
;; ORGANISM: Pseudomonas aeruginosa
US-09-865-159-18

Query Match 12.9%; Score 83; DB 5; Length 175;
Best Local Similarity 27.2%; Pred. No. 1.2;
Matches 37; Conservative 18; Mismatches 57; Indels 24; Gaps 8;

QY 1 ALE---GTEFARTQVRAVEVSALKTAAESALTEKEIYSSAPKDTQYDIFGFTSTLL 57
Db 44 ALEKGGGGEFARQLESRMTLASGLTKYSDIFSQ-----DGSCTPANTATAGIEKDT-- 96
QY 58 DSGKSGQIOYTDN---KQGTVELVATLGRSS-GSAIKGAVITV---SRKNDGVNCKI 108
Db 97 DINGKRYAVATGGTAAAGGCTIVATMKASDVATPLRGKTLTLTLGNMADKSGYTWAC--- 154
QY 109 TKPTTAKRPYAPANC 124
Db 155 ---TSNA-DNKYLPKTC 167

RESULT 11
US-09-865-159-16
; Sequence 16, Application US/09865159
; GENERAL INFORMATION:
; APPLICANT: Irvia, Randall T.
; APPLICANT: Hodges, Robert S.
; TITLE OF INVENTION: PSEUDOMONAS TREATMENT
; FILE OF INVENTION: COMPOSITION AND METHOD
; FILE REFERENCE: 8900-0008.30
; CURRENT APPLICATION NUMBER: US/09/865,159
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329,884
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 175
; TYPE: PR1
; ORGANISM: Pseudomonas aeruginosa
US-09-865-159-16

Query Match 12.7%; Score 81.5; DB 5; Length 175;
Best Local Similarity 26.2%; Pred. No. 1.7;
Matches 34; Conservative 18; Mismatches 57; Indels 21; Gaps 7;
QY 4 GTEFARTQVRAVEVSALKTAAESALTEKEIYSSAPKDTQYDIFGFTSTLLDGSCKS 63
Db 50 GGEFARQLESRMTLASGLTKYSDIFSQ-----DGSCTPANTATAGIEKDT--DINGKY 102
QY 64 QIOYTDN---KQGTVELVATLGRSS-GSAIKGAVITV---SRKNDGVNCKITKPTTA 114
Db 103 VAKVTTGGTAAAGGCTIVATMKASDVATPLRGKTLTLTLGNMADKSGYTWAC---TSNA 158
QY 115 WKPYAPANC 124
Db 159 -DNKYLPKTC 167

RESULT 12

US-09-696-188B-19
; Sequence 19, Application US/09696188B
; GENERAL INFORMATION:
; APPLICANT: Stewart, C. Neal
; McKee, Marian L.
; O'Brien, Alison D.
; Wachtel, Marian R.

TITLE OF INVENTION: Method of Stimulating An Immune Response
By Administration of Host Organisms That Express Intim
Alone Or As A Fusion Protein With One Or More Other
Antigens.

NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSER: Finnegan, Henderson, Farabow, Garrett &
Dunner, L.L.P.
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA

ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/696,188B
FILING DATE: 26-Oct-2000
CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/840,466
FILING DATE: 1997-04-18

ATTORNEY/AGENT INFORMATION:
NAME: Boone, Laurel S.
REGISTRATION NUMBER: 43,505
REFERENCE/DOCKET NUMBER: 04995,0029-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400

INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 934 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-696-188B-19

Query Match 12.3%; Score 79; DB 5; Length 934;
Best Local Similarity 25.6%; Pred. No. 24;
Matches 33; Conservative 19; Mismatches 47; Indels 30; Gaps 7;

QY 11 QVTRAVEVSALKTAAESALTEKEIYSSAPKDTQYDIFGFTSTLLD-GSGK 62
Db 655 QTASISFELIADKT---TAVANGKDAIKTYVKKMGQPVNNO---SYFSTNGFNGK 708
QY 63 SQIOYTDNKGTEVELVAT---LGR-----SSGSAIKGAVITV---VSRKNDGVNCK 106
Db 709 SQIOATGTGNGRATITLTSSAGKATVSAIVSGCAEVKATEVTFPELKDINKVDIIGNN 768
QY 107 KIITKPTAW 115
Db 769 VNGELPNIW 777

RESULT 13
US-09-999-201-3
; Sequence 3, Application US/09999201
; GENERAL INFORMATION:
; APPLICANT: Randy M. Berka
; APPLICANT: Michael W. Rey

APPLICANT: Kimberly Brown
TITLE OF INVENTION: Promoters for Expressing Genes In A
FILE OF INVENTION: Fungal Cell
FILE REFERENCE: 5611.200-US
CURRENT APPLICATION NUMBER: US/09/999,201
CURRENT FILING DATE: 2001-10-30
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/534,407
PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 581
TYPE: PRN
ORGANISM: Fusarium
US-09-999-201-3

Query Match 11.7%; Score 75; DB 5; Length 581;
Best Local Similarity 21.5%; Pred. No. 31;
Matches 35; Conservative 24; Mismatches 40; Indels 64; Gaps 8;

QY 3 EGTETARTOYTRAVSEVSALEKTAESAILEGKEIVSATPRDYOYDIGFTSTLLDGSCK 62
DB 387 KGYAKKTKTKET--IAAKTYADGFV---AVQYTPKDGSLAEQDKST---GAPK 437
QY 63 SOIOY-----TDNKGDTVELVATLGKSSGSAIKG-----AVTVSRKN--- 100
DB 438 SAVHLTWSYAFAVATTEHRDGIIS--PSMGESSANKVPACQADCTTFESVKNVOV 495
QY 101 -----DGVNCKITKTP 113
DB 496 SSDOKVYVGVSVTELNNSPDGIALTPSSGGSWSVKV-KIPS 537

RESULT 14
US-09-708-427-4849
Sequence 4849, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4849
LENGTH: 857
TYPE: PRN
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc.feature
LOCATION: 1..857
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc.feature
LOCATION: 1..857
OTHER INFORMATION: Ceres Seq. ID 1813236
US-09-708-427-4849

Query Match 11.7%; Score 75; DB 5; Length 857;
Best Local Similarity 25.2%; Pred. No. 50;
Matches 36; Conservative 19; Mismatches 56; Indels 32; Gaps 5;

QY 1 ALEGTETARTOYTRAVSEVSALEKTAESAILEGKEIVS-----ATPKDYOYDIGFTST 55
DB 673 ALENNEKLTQFSSAVS-----TLLSDVSSNREIISIDNSLODKRASTDV---NST 723
QY 56 LLDGSGKSOIOYTDNKGDTVELVATLGKSSGSAIKGAVTVSR-----KNDG 102
DB 724 IVPCESENKELRTHHDDNVVEIKONTGKCLGHEYK-----VTRFDFLYNHHIYMIELDK 778
QY 103 VVNCKITKTPPTAMKPNVAPANCP 125

DB 779 IVNRRLNSLKTSTOYDEATSTP 801

RESULT 15
US-09-708-427-4848
Sequence 4848, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPT
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4848
LENGTH: 931
TYPE: PRN
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc.feature
LOCATION: 1..931
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc.feature
LOCATION: 1..931
OTHER INFORMATION: Ceres Seq. ID 1813235
US-09-708-427-4848

Query Match 11.7%; Score 75; DB 5; Length 931;
Best Local Similarity 25.2%; Pred. No. 56;
Matches 36; Conservative 19; Mismatches 56; Indels 32; Gaps 5;

QY 1 ALEGTETARTOYTRAVSEVSALEKTAESAILEGKEIVS-----ATPKDYOYDIGFTST 55
DB 747 ALENNEKLTQFSSAVS-----TLLSDVSSNREIISIDNSLODKRASTDV---NST 797
QY 56 LLDGSGKSOIOYTDNKGDTVELVATLGKSSGSAIKGAVTVSR-----KNDG 102
DB 798 IVPCESENKELRTHHDDNVVEIKONTGKCLGHEYK-----VTRFDFLYNHHIYMIELDK 852
QY 103 VVNCKITKTPPTAMKPNVAPANCP 125
DB 853 IVNRRLNSLKTSTOYDEATSTP 875

Search completed: February 8, 2002, 15:26:39
Job time: 204 sec

Fri Feb 8 15:44:55 2002

us-09-865-159-8.rapn

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 8, 2002, 15:24:32 ; Search time 67.74 Seconds
(without alignments)
138.874 Million cell updates/sec

Title: US-09-865-159-10

Perfect score: 654
Sequence: 1 ALEGTFFSSQVSRVMAENG.....GGWSCATVDAKFRPNCITD 127

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_1101:*

- 1: /SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:*
- 2: /SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*
- 3: /SIDS8/gcgdata/geneseq/geneseqp/AA1982.DAT:*
- 4: /SIDS8/gcgdata/geneseq/geneseqp/AA1983.DAT:*
- 5: /SIDS8/gcgdata/geneseq/geneseqp/AA1984.DAT:*
- 6: /SIDS8/gcgdata/geneseq/geneseqp/AA1985.DAT:*
- 7: /SIDS8/gcgdata/geneseq/geneseqp/AA1986.DAT:*
- 8: /SIDS8/gcgdata/geneseq/geneseqp/AA1987.DAT:*
- 9: /SIDS8/gcgdata/geneseq/geneseqp/AA1988.DAT:*
- 10: /SIDS8/gcgdata/geneseq/geneseqp/AA1989.DAT:*
- 11: /SIDS8/gcgdata/geneseq/geneseqp/AA1990.DAT:*
- 12: /SIDS8/gcgdata/geneseq/geneseqp/AA1991.DAT:*
- 13: /SIDS8/gcgdata/geneseq/geneseqp/AA1992.DAT:*
- 14: /SIDS8/gcgdata/geneseq/geneseqp/AA1993.DAT:*
- 15: /SIDS8/gcgdata/geneseq/geneseqp/AA1994.DAT:*
- 16: /SIDS8/gcgdata/geneseq/geneseqp/AA1995.DAT:*
- 17: /SIDS8/gcgdata/geneseq/geneseqp/AA1996.DAT:*
- 18: /SIDS8/gcgdata/geneseq/geneseqp/AA1997.DAT:*
- 19: /SIDS8/gcgdata/geneseq/geneseqp/AA1998.DAT:*
- 20: /SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:*
- 21: /SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT:*
- 22: /SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	654	100.0	127	AAV44379	Exemplary truncate
2	186.5	28.5	127	AAV44378	Exemplary truncate
3	147	22.5	123	AAV44376	Exemplary truncate
4	133.5	20.4	122	AAV44377	Exemplary truncate
5	128.5	19.6	169	AAV44381	Exemplary truncate
6	127	19.4	169	AAV44380	Exemplary truncate
7	123	18.8	129	AAV44375	Exemplary truncate
8	115	17.6	168	AAV44385	Exemplary truncate
9	113.5	17.4	168	AAV44384	Exemplary truncate
10	106.5	16.3	82	AAV44384	Exemplary truncate
11	104.5	16.0	175	AAV44383	Exemplary truncate

12	103	15.7	175	AAV44382	P. aeruginosa H co
13	97.5	14.9	69	AAV44382	B. nodosus pilin p
14	96	14.7	17	AAV44382	P. aeruginosa K87 p
15	96	14.7	17	AAV44382	Pilin derived pep
16	96	14.7	17	AAV44382	Cell surface bindi
17	87	13.3	471	AAV44382	Cellulolyticase
18	87	13.3	471	AAV44382	T. longibrachiatum
19	84	12.8	471	AAV44382	Trichoderma cellulo
20	83	12.7	279	AAV44382	Proteinase K varia
21	83	12.7	449	AAV44382	Cellulomonas fimi
22	81.5	12.5	1569	AAV44382	E. coli growth and
23	81	12.4	14	AAV44382	K87 polypeptide de
24	81	12.4	387	AAV44382	Endoglucanase prot
25	79	12.1	610	AAV44382	Ligand binding dom
26	78	11.9	209	AAV44382	C glutamicum prote
27	77.5	11.9	184	AAV44382	White spot syndrom
28	77.5	11.9	204	AAV44382	Shrimp white spot
29	77.5	11.9	22	AAV44382	White spot syndrom
30	77.5	11.9	264	AAV44382	Sequence of Ag513
31	77	11.8	525	AAV44382	C glutamicum prote
32	76.5	11.7	303	AAV44382	Dac gv (clone 259)
33	76	11.6	876	AAV44382	Human cytoskeletal
34	75.5	11.5	246	AAV44382	IL-6 binding inhib
35	75	11.5	14	AAV44382	C-terminal pilin p
36	75	11.5	1700	AAV44382	Plasmodium falcipt
37	74.5	11.4	201	AAV44382	Arabidopsis thalia
38	74.5	11.4	201	AAV44382	Arabidopsis thalia
39	74.5	11.4	233	AAV44382	Arabidopsis thalia
40	74	11.3	240	AAV44382	Human TF anti-Idio
41	74	11.3	293	AAV44382	Sequence of Trifir
42	74	11.3	338	AAV44382	Endoglucanase prot
43	73.5	11.2	280	AAV44382	Merozoite surface a
44	73.5	11.2	381	AAV44382	Streptomyces livid
45	73.5	11.2	381	AAV44382	Rhodothermus marin

ALIGNMENTS

RESULT 1	AAV44379	standard; Protein: 127 AA.
ID	AAV44379	
AC	AAV44379;	
XX		
DT	14-MAR-2000	(first entry)
XX		
DE	Exemplary truncated P. aeruginosa K87 pilin protein.	
XX		
KW	Modified K87 pilin protein: alpha-helical forming portion;	
KW	Pseudomonas infection; cystic fibrosis; neutropenia.	
XX		
OS	Pseudomonas aeruginosa.	
XX		
PN	WO965511-A2.	
XX		
PD	23-DEC-1999.	
XX		
PF	11-JUN-1999;	99WO-CA00554.
XX		
PR	12-JUN-1998;	98US-0089155.
XX		
PA	(UNAL-) UNTV ALBERTA.	
XX		
PI	Hodges RS, Irvin RT;	
XX		
DR	WPI: 2000-106013/09.	
XX		
XX	N-PSDB: AA229538.	
PT	Composition for treating or preventing Pseudomonas aeruginosa infection	
PT	compositing pilin protein that can not self-assemble	
XX		
PS	Claim 9; Fig 1E; 32pp; English.	

XX The present sequence is the modified KB7 pilin protein from
 CC P.aeruginosa. The N-terminal peptide region preferably lacks the first
 CC 15-40 residues of native P.aeruginosa. Modified pilin proteins are
 CC prepared by PCR amplification of pilin coding sequences using primers
 CC that effect the desired deletion, modification or insertion of a coiled-
 CC coil moiety in the coding sequences. The modified protein thus lacks a
 CC critical alpha-helical forming portion. This prevents oligomerisation of
 CC pilin protein necessary for attachment to the host cell during infection.
 CC The ligated plasmid DNA was transformed into an expression host. The
 CC modified pilin protein is useful in treatment and prophylaxis for
 CC individuals at risk of Pseudomonas infection, e.g. cystic fibrosis
 CC patients, burn patients, and severe neutropenic patients.

XX Sequence 127 AA;

Query Match 100.0%; Score 654; DB 21; Length 127;
 Best Local Similarity 100.0%; Pred. No. 1.5e-58;
 Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALESTFSSQVSRVMAEAGSLKTAVEACLDGRTAVGTAAGCCDPCATGSSLLTGASQT 60
 Db 1 aalegtfssrqvsvrmaeagslktaveaclodgrtavgtaagccdpagatgsslltgasqt 60
 QY 61 SQTLPNTGVPVLDPLTQTTLIAFTNGASAAISGQTLTWRDVGWGCATVDAK 120
 Db 61 sqtlpntgvpvldplqtltlftngasaaaisgqtlwtrdvngwscatvdakf 120
 QY 121 RPNCGTD 127
 Db 121 rpnctd 127

RESULT 2
 AA44378
 ID AAY44378 standard; Protein: 127 AA.

AC AAY44378;

DT 14-MAR-2000 (first entry)

DE Exemplary truncated P. aeruginosa P1 pilin protein.

KW Modified P1 pilin protein; alpha-helical forming portion;

KW Pseudomonas infection; cystic fibrosis; neutropenia.

OS Pseudomonas aeruginosa.

PN W09965511-A2.

PD 23-DEC-1999.

PE 11-JUN-1999; 99WO-CA00554.

PR 12-JUN-1998; 98US-0089155.

PA (UYAL-) UNIV ALBERTA.

PI Hodges RS, Irvin RT;

DR WPI: 2000-106013/09.

XX N-PSDB; AA229537.

PT Composition for treating or preventing Pseudomonas aeruginosa infection

XX comprising pilin protein that can not self-assemble -

XX Claim 9; Fig 1D; 32pp; English.

CC The present sequence is the modified P1 pilin protein from
 CC P.aeruginosa. The N-terminal peptide region preferably lacks the first
 CC 15-40 residues of native P.aeruginosa. Modified pilin proteins are
 CC prepared by PCR amplification of pilin coding sequences using primers

CC that effect the desired deletion, modification or insertion of a coiled-
 CC coil moiety in the coding sequences. The modified protein thus lacks a
 CC critical alpha-helical forming portion. This prevents oligomerisation of
 CC pilin protein necessary for attachment to the host cell during infection.
 CC The ligated plasmid DNA was transformed into an expression host. The
 CC modified pilin protein is useful in treatment and prophylaxis for
 CC individuals at risk of Pseudomonas infection, e.g. cystic fibrosis
 CC patients, burn patients, and severe neutropenic patients.

XX Sequence 127 AA;

Query Match 28.5%; Score 186.5; DB 21; Length 127;
 Best Local Similarity 35.4%; Pred. No. 2.2e-11;
 Matches 45; Conservative 25; Mismatches 44; Indels 13; Gaps 3;

QY 1 ALEGTFSRQVSRVMAEAGSLKTAVEACLDGRTAVGTAAGCCDPCATGSSLLTGCA 57
 Db 1 aalegtfartqytravsevsalktaeasalegkeivssatpdktdydgflestlldgs 60
 QY 58 SQTSLPNTGVPVLDPLTQTTLIAFTNGASAAISGQTLTWRDVGWGC-ATTV 116
 Db 61 gksq-----iqvtdnkdgqlveivatlqgssgalkgaviltsrkdngwcnkckkt 111
 QY 117 DAKFRPN 123
 Db 112 ptawkpn 118

RESULT 3
 AAY44376
 ID AAY44376 standard; Protein: 123 AA.

AC AAY44376;

DT 14-MAR-2000 (first entry)

DE Exemplary truncated P. aeruginosa PAK pilin protein.

KW Modified PAK pilin protein; alpha-helical forming portion;

KW Pseudomonas infection; cystic fibrosis; neutropenia.

OS Pseudomonas aeruginosa.

PN W09965511-A2.

PD 23-DEC-1999.

PE 11-JUN-1999; 99WO-CA00554.

PR 12-JUN-1998; 98US-0089155.

PA (UYAL-) UNIV ALBERTA.

PI Hodges RS, Irvin RT;

DR WPI: 2000-106013/09.

XX N-PSDB; AA229535.

PT Composition for treating or preventing Pseudomonas aeruginosa infection

XX comprising pilin protein that can not self-assemble -

XX Claim 9; Fig 1B; 32pp; English.

CC The present sequence is the modified PAK pilin protein from
 CC P.aeruginosa. The N-terminal peptide region preferably lacks the first
 CC 15-40 residues of native P.aeruginosa. Modified pilin proteins are
 CC prepared by PCR amplification of pilin coding sequences using primers
 CC that effect the desired deletion, modification or insertion of a coiled-
 CC coil moiety in the coding sequences. The modified protein thus lacks a
 CC critical alpha-helical forming portion. This prevents oligomerisation of
 CC pilin protein necessary for attachment to the host cell during infection.
 CC The ligated plasmid DNA was transformed into an expression host. The

CC modified pilin protein is useful in treatment and prophylaxis for
CC individuals at risk of Pseudomonas infection, e.g. cystic fibrosis
CC patients, burn patients, and severe neutropenic patients.
XX
SQ Sequence 123 AA;

Query Match 22.5%; Score 147; DB 21; Length 123;
Best Local Similarity 33.8%; Pred. No. 2e-07;
Matches 44; Conservative 16; Mismatches 58; Indels 12; Gaps 5;

OY 1 ALEGEFSRSQVSRVMAAGSLKTAVEACLODGG---RTAVGTAAGCCDPGATGSSLLTGA 57
DB 1 alegetefarsqasalaasvnpklktveealsrgwsvksqgtl-----edatlkkevplgv 54
OY 58 SQTSLPTNTNGVPOVLDPLTQTITATFNGASAAISGQTLTWRD-VNCGMGCATTV 116
DB 55 aadankigtialkpdadg-taditliltmg-gagphnkylilrltraadglwactsdg 112
OY 117 DAKFRPNCCT 126
DB 113 deqfipkqcs 122

RESULT 4

AAV44377
ID AAY44377 standard; Protein; 122 AA.

XX
AC AAY44377;

XX
DT 14-MAR-2000 (first entry)

XX
DE Exemplary truncated P. aeruginosa PAO pilin protein.

XX
KW Modified PAO pilin protein; alpha-helical forming portion;

XX
KM Pseudomonas infection; cystic fibrosis; neutropenia.

XX
OS Pseudomonas aeruginosa.

XX
PN WO9965511-A2.

XX
PD 23-DEC-1999.

XX
PF 11-JUN-1999; 99WO-CA00554.

XX
PR 12-JUN-1998; 98US-0089155.

XX
PA (UYAL-) UNIV ALBERTA.

XX
PI Hodges RS, Irvin RT;

XX
DR WPI: 2000-106013/09.

XX
DR N-PSDB; AA229536.

XX
PT Composition for treating or preventing Pseudomonas aeruginosa infection

XX
PS comprising pilin protein that can not self-assemble -

XX
PS Claim 9; Fig 1C; 32pp; English.

CC The present sequence is the modified PAO pilin protein from
CC P. aeruginosa. The N-terminal peptide region preferably lacks the first
CC 15-40 residues of native P. aeruginosa. Modified pilin proteins are
CC prepared by PCR amplification of pilin coding sequences using primers
CC that effect the desired deletion, modification or insertion of a coiled-
CC coil moiety in the coding sequences. The modified protein thus lacks a
CC critical alpha-helical forming portion. This prevents oligomerisation of
CC pilin protein necessary for attachment to the host cell during infection.
CC The ligated plasmid DNA was transformed into an expression host. The
CC modified pilin protein is useful in treatment and prophylaxis for
CC individuals at risk of Pseudomonas infection, e.g. cystic fibrosis
CC patients, burn patients, and severe neutropenic patients.
XX
SQ Sequence 122 AA;

Query Match 20.4%; Score 133.5; DB 21; Length 122;
Best Local Similarity 31.8%; Pred. No. 4.6e-06;
Matches 41; Conservative 17; Mismatches 56; Indels 15; Gaps 4;

OY 1 ALEGEFSRSQVSRVMAAGSLKTAVEACLODGG---RTAVGTAAGCCDPGATGSSLLTGA 56
DB 1 alegetefarsqasalaatnplktveeslrglsgskikglta-----stateyag 54
OY 57 ASQTSQTLPTNTNGVPOVLDPLTQTITATFNGASAAISG-QTLTWRDVGWGCATT 115
DB 55 vepdanxl-----gvlaavedsgagdlftlqtgtspxnakviltlntraadgvaackst 110
OY 116 VDAKFRPNC 124
DB 111 qdpmftpkq 119

RESULT 5

AAV44381
ID AAY44381 standard; Protein; 169 AA.

XX
AC AAY44381;

XX
DT 14-MAR-2000 (first entry)

XX
DE P. aeruginosa E coil-truncated PAK pilin protein.

XX
KW Modified PAK pilin protein; alpha-helical forming portion; E coil;

XX
KM Exemplary coil; coiled coil heterodimer; host cell-receptor site;

XX
KM Pseudomonas infection; cystic fibrosis; neutropenia.

XX
OS Pseudomonas aeruginosa.

XX
PN WO9965511-A2.

XX
PD 23-DEC-1999.

XX
PF 11-JUN-1999; 99WO-CA00554.

XX
PR 12-JUN-1998; 98US-0089155.

XX
PA (UYAL-) UNIV ALBERTA.

XX
PI Hodges RS, Irvin RT;

XX
DR WPI: 2000-106013/09.

XX
DR N-PSDB; AA229540.

XX
PT Composition for treating or preventing Pseudomonas aeruginosa infection

XX
PS comprising pilin protein that can not self-assemble -

XX
PS Claim 1; Fig 3B; 32pp; English.

CC The present sequence encodes E coil truncated PAK pilin protein from
CC P. aeruginosa. The first 15-40 residues of the N-terminal peptide region
CC is replaced by a peptide segment capable of forming a coiled-coil
CC heterodimer with an oppositely charged peptide segment which can form
CC dimeric structures. These proteins are less inflammatory due to reduced
CC degree of mobilisation of pilin protein necessary for attachment to the host
CC cell during infection. The modified pilin protein is useful in treatment
CC and prophylaxis for individuals at risk of Pseudomonas infection,
CC e.g. cystic fibrosis patients, burn patients, and severe neutropenic
CC patients.
XX
SQ Sequence 169 AA;

Query Match 19.6%; Score 128.5; DB 21; Length 169;
Best Local Similarity 32.3%; Pred. No. 2.2e-05;
Matches 43; Conservative 16; Mismatches 59; Indels 15; Gaps 6;

QY 1 ALE---GTEFSRSQVSRVMAEAGSLKTAVEACLODG---RTAVGTAAQCQDPGATGSSLL 54
 Db 44 alexg9ggefataresegasalasvnpklttveealsrgvsksgtgt-----edatkvevp 97
 QY 55 TGASQTSQTLPTNTGVPQVLDPLTQTITIAFNGASAAISQOTLTWTRD-VNGGWSCA 113
 Db 98 lgvadanklgtlalkpdpadg-faditlftmg-gagpkngkklitlrrtaadglwkt 155
 QY 114 TTVDAKFRPNCGT 126
 Db 156 sdgdeqfipkqcs 168

RESULT 6
 ID AAY44380 standard; Protein; 169 AA.
 AC AAY44380;
 XX
 DT 14-MAR-2000 (first entry)
 DE P. aeruginosa H coil-truncated PAK pilin protein.
 XX
 KW Modified PAK pilin protein; alpha-helical forming portion;
 KM coiled coil homodimer; host cell-receptor site; Pseudomonas infection;
 KM cystic fibrosis; neutropenia.
 XX
 OS Pseudomonas aeruginosa.
 XX
 PN W09965511-A2.
 XX
 PD 23-DEC-1999.
 XX
 PF 11-JUN-1999; 99WO-CA00554.
 XX
 PR 12-JUN-1998; 98US-0089155.
 XX
 PA (UYAL-) UNIV ALBERTA.
 XX
 PI Hodges RS, Irvin RT;
 XX
 DR WPI: 2000-106013/09.
 DR N-PSDB; AA229539.
 XX
 XX

Composition for treating or preventing Pseudomonas aeruginosa infection
 comprising pilin protein that can not self-assemble -
 Claim 1; Fig 3A; 32pp; English.

The present sequence is the H coil truncated PAK pilin protein from
 CC P. aeruginosa. The first 15-40 residues of the N-terminal peptide region
 CC is replaced by a peptide segment capable of forming a coiled-coil
 CC homodimer with an identical peptide segment which can form dimeric
 CC structures. These proteins are less inflammatory due to reduced degree of
 CC mobilisation of host-cell receptor sites. This prevents oligomerisation
 CC of pilin protein necessary for attachment to the host cell during
 CC infection. The modified pilin protein is useful in treatment and
 CC prophylaxis for individuals at risk of Pseudomonas infection,
 CC e.g. cystic fibrosis patients, burn patients, and severe neutropenic
 CC patients.
 CC
 XX

Sequence 169 AA;

Query Match 19.4%; Score 127; DB 21; Length 169;
 Best Local Similarity 31.5%; Pred. No. 3.2e-05;
 Matches 40; Conservative 16; Mismatches 59; Indels 12; Gaps 5;

QY 4 GTEFSRSQVSRVMAEAGSLKTAVEACLODG---RTAVGTAAQCQDPGATGSSLLTGASQ 60
 Db 50 ggeatarsegasalasvnpklttveealsrgvsksgtgt-----edatkveplgyaad 103

QY 61 SQTLPNTGVPQVLDPLTQTITIAFNGASAAISQOTLTWTRD-VNGGWSCATTVDAK 119
 Db 104 ankigtalrpdpadg-faditlftmg-gagpkngkklitlrrtaadglwktsgdq 161
 QY 120 FRPNCGT 126
 Db 162 fipkqcs 168

RESULT 7
 ID AAY44375 standard; Protein; 129 AA.
 AC AAY44375;
 XX
 DT 14-MAR-2000 (first entry)
 DE Exemplary truncated P. aeruginosa K122 pilin protein.
 XX
 KW Modified K122 pilin protein; alpha-helical forming portion;
 KM Pseudomonas infection; cystic fibrosis; neutropenia.
 XX
 OS Pseudomonas aeruginosa.
 XX
 PN W09965511-A2.
 XX
 PD 23-DEC-1999.
 XX
 PF 11-JUN-1999; 99WO-CA00554.
 XX
 PR 12-JUN-1998; 98US-0089155.
 XX
 PA (UYAL-) UNIV ALBERTA.
 XX
 PI Hodges RS, Irvin RT;
 XX
 DR WPI: 2000-106013/09.
 DR N-PSDB; AA229534.
 XX
 XX

Composition for treating or preventing Pseudomonas aeruginosa infection
 comprising pilin protein that can not self-assemble -
 Claim 9; Fig 1A; 32pp; English.

The present sequence is the modified K122 pilin protein from
 CC P. aeruginosa. The N-terminal 1-28 residues are deleted from K122 strain
 CC pilin protein. The modified protein thus lacks a critical alpha-helical
 CC forming portion. This prevents oligomerisation of pilin protein necessary
 CC for attachment to the host cell during infection. The first five
 CC amino acid residues are not native to the K122 sequence, but are derived
 CC from an intrinsic coding sequence of the expression vector. The
 CC C-terminal residue is the Pro residue immediately upstream of the stop
 CC OCH codons. The modified pilin protein is useful in treatment and
 CC prophylaxis for individuals at risk of Pseudomonas infection, e.g.
 CC cystic fibrosis patients, burn patients, and severe neutropenic patients.
 CC
 XX

Sequence 129 AA;

Query Match 18.8%; Score 123; DB 21; Length 129;
 Best Local Similarity 30.7%; Pred. No. 5.7e-05;
 Matches 42; Conservative 20; Mismatches 47; Indels 26; Gaps 7;

QY 1 ALGTEFSRSQVSRVMAEAGSLKTAVEACLODGRRTAVGTAAQ---QCDPGATG---SSL 53
 Db 1 alegtetaqlsemltlasgltkvsdfsgqscpantaatagiekddingkyavkv 60
 QY 54 LTGASQTSQTLPTNTGVPQVLDPLTQTITIAFNGASAAISQOTLTWTRD-VNGG-- 109
 Db 61 ttggttaa-----sggcttvaumkasdvaclprgkltlilgnadkgsy 104
 QY 110 -MSCATTVDAKFRPNCGT 125
 Db 110 -MSCATTVDAKFRPNCGT 125


```

XX DE B. nodosus pilin protein submolecular unit.
XX PI
XX XX Antibodies: whole pili binding; basis; vaccine; bacterial infection;
XX KW runniant footrot infection; sheep; type IV pillated bacteria.
XX XX
XX OS Bacteroides nodosus.
XX PN
XX PD WO9311791-A.
XX PD 24-JUN-1993.
XX PF 17-DEC-1992; 92WO-US11085.
XX PR 18-DEC-1991; 91US-0809762.
XX XX
XX PA (UYOR-) UNIV OREGON HEALTH SCI.
XX PI Smith AW;
XX DR WPI; 1993-213824/26.
XX PT Antigenic preparation - stimulates production of antibodies binding
XX PT to pilin protein of type IV pillated bacteria, useful in
XX PT vaccine compsn.
XX PS Claim 3; Page 24; 44pp; English.
XX CC The sequence is that of a submolecular unit of Bacteroides nodosus
XX CC pilin protein which corresponds to at least one epitope common to
XX CC structural pilin proteins of Type IV pillated bacteria. It is
XX CC capable of eliciting antibodies (Abs) which bind to whole pili of
XX CC type IV bacteria. The ability of the submolecular unit to produce
XX CC Abs which bind to whole pili provides the basis for vaccines against
XX CC type IV bacterial infections, e.g. footrot infection in ruminants.
XX SQ Sequence 82 AA;

Query Match 16.3%; Score 106.5; DB 14; Length 82;
Best Local Similarity 42.4%; Pred. No. 0.0015;
Matches 25; Conservative 8; Mismatches 21; Indels 5; Gaps 1;

OY 8 SRSQVSRVAEAGSLKTAWEACLODGRNAVGTAAQCQCPGATGSSLLTGASQTSQTLPT 66
   :|||||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 29 arsqvsvmsecgmrtatetcltdgk-----egkdcfigwtltsnllcstdvdekfpt 82

RESULT 11
AAV44383
ID AAV44383 standard; Protein; 175 AA.
XX AC
XX AC AAV44383;
XX DT 14-MAR-2000 (first entry)
XX DE P. aeruginosa E coil-truncated K122 pilin protein.
XX KW Modified K122 pilin protein; alpha-helical forming portion; E coil;
XX KW Exemplary coil; coiled coil homodimer; host cell-receptor site;
XX KW Pseudomonas infection; cystic fibrosis; neutropenia.
XX OS Pseudomonas aeruginosa.
XX PN
XX PN WO9965511-A2.
XX PD 23-DEC-1999.
XX PF 11-JUN-1999; 99WO-CA00554.
XX PR 12-JUN-1998; 98US-0089155.
XX PA (UYAL-) UNIV ALBERTA.
XX PI
XX DR

```

```

XX XX
XX PI Hodges RS, Irvin RT;
XX XX
XX DR WPI: 2000-106013/09.
XX DR N-PSDB; AAZ29542.
XX XX
XX PT Composition for treating or preventing Pseudomonas aeruginosa infection
XX PT comprising pilin protein that can not self-assemble.
XX PS Claim 1; Fig 4B; 32pp; English.
XX CC The present sequence encodes E coil truncated K122 pilin protein from
XX CC P. aeruginosa. The first 15-40 residues of the N-terminal peptide region
XX CC is replaced by a peptide segment capable of forming a coiled-coil
XX CC heterodimer with an oppositely charged peptide segment which can form
XX CC dimeric structures. These proteins are less inflammatory due to reduced
XX CC degree of mobilisation of host-cell receptor sites. This prevents
XX CC oligomerisation of pilin protein necessary for attachment to the host
XX CC cell during infection. The modified pilin protein is useful in treatment
XX CC and prophylaxis for individuals at risk of Pseudomonas infection,
XX CC e.g. cystic fibrosis patients, burn patients, and severe neutropenic
XX CC patients.
XX SQ Sequence 175 AA;

```

```

Query Match 16.0%; Score 104.5; DB 21; Length 175;
Best Local Similarity 29.3%; Pred. No. 0.0061;
Matches 41; Conservative 20; Mismatches 48; Indels 31; Gaps 8;

OY 1 ALE---GTEFRSQVSRMAEAGSLKTAWEACLODGRNAVGTAG---OCPCGATG--- 50
   |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 44 aleksgggetarqqlsermlasgltkvsdlfsqdsdpantatagiekddingkyv 103

OY 51 SLLTGASQTSQTLPTNTGVGPQVLDPLTTQTTLATF-GNGASAAISGQTLTWT-RDVNG 108
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 104 akvttygtaaa-----sgctivatkasadvapirgkcltcltlgnadk 147

OY 109 G---WSCATTVDAKFRPNC 125
   ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 148 gsytwactsnadnkylpdkc 167

RESULT 12
AAV44382
ID AAV44382 standard; Protein; 175 AA.
XX AC
XX AC AAV44382;
XX DT 14-MAR-2000 (first entry)
XX DE P. aeruginosa H coil-truncated K122 pilin protein.
XX KW Modified K122 pilin protein; alpha-helical forming portion;
XX KW coiled coil homodimer; host cell-receptor site; Pseudomonas infection;
XX KW cystic fibrosis; neutropenia.
XX OS Pseudomonas aeruginosa.
XX PN
XX PN WO9965511-A2.
XX PD 23-DEC-1999.
XX PF 11-JUN-1999; 99WO-CA00554.
XX PR 12-JUN-1998; 98US-0089155.
XX PA (UYAL-) UNIV ALBERTA.
XX PI Hodges RS, Irvin RT;
XX PI
XX DR WPI: 2000-106013/09.
XX DR N-PSDB; AAZ29541.

```

PS Claim 3; page 24; 44pp; English.

Sequence	17 AA
SQ	

Query match	14.7%;	Score 96;	DB 13;	Length 17;
-------------	--------	-----------	--------	------------

Best Local Similarity 100.0%; Pred. No. 0.0024;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 111 SCATTVDKFRPNCCTD 127
 ||||||||||||||||
 Db 1 scattvdakfirpncctd 17

Search completed: February 8, 2002, 15:24:33
 Job time: 78 sec

RESULT 15

AAR86706

ID AAR86706 standard; peptide: 17 AA.

AC AAR86706;

DT 26-JUN-1996 (first entry)

DE Piliin derived peptide, KB7.

KW Epitope: exoenzyme; ExoS: enzymatic/cytotoxic protein; PK99H; MCA1;
 KW P. aeruginosa; adhesin; monoclonal antibody; buccal epithelial cell;
 KW cell surface receptor; adhesion domain; piliin protein; vaccine;
 KW immunisation; infection; targeted drug delivery; carcinoma;
 KW pulmonary epithelial cell.

OS Pseudomonas aeruginosa.

PN US5468484-A.

PD 21-NOV-1995.

PF 25-JUN-1991; 91US-0721759.

PR 28-JUN-1993; 93US-0084739.

PR 25-JUN-1991; 91US-0721759.

PA (SPIS-) SPI SYNTHETIC PEPTIDES INC.

PI Hodges RS, Irvin RT, Paranchych W, Sokol PA, Woods DE;

DR WPI: 1996-010050/01.

PT Preventing P. aeruginosa infections by passive immunisation - using
 PT monoclonal antibody reactive with exos and piliin peptide epitope(s)
 PS Claim 1; Column 33; 26pp; English.

CC The sequences given in AAR86702-08 are peptides which have the same
 CC immunoreactivity as the peptide sequence given in AAR86701. These
 CC peptides are derived from the P. aeruginosa piliin protein. The peptide
 CC of the invention is derived from the exoenzyme, ExoS. ExoS is an
 CC enzymatic/cytotoxic protein present on the surface of P. aeruginosa
 CC cells. It is also an adhesin. It demonstrates immunospecific binding
 CC to monoclonal antibodies PK99H and MCA1. The ExoS derived peptide has
 CC by blocking a cell surface receptor. It is homologous to known adhesion
 CC domains in the P. aeruginosa piliin protein, esp. the region 131-143.
 CC These peptides may be used in vaccines to provide active immunisation
 CC against infection by P. aeruginosa or related organisms. They can also
 CC be used for targeted drug delivery to pulmonary epithelial cells, e.g.
 CC for treating carcinoma they are coupled to photoactivatable
 CC chemotherapeutic agents.

SQ Sequence 17 AA;

Query Match

Best Local Similarity 14.7%; Score 96; DB 17; Length 17;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 111 SCATTVDKFRPNCCTD 127

Db 1 scattvdakfirpncctd 17

Fri Feb 8 15:44:47 2002

us-09-865-159-10.rag

C:Genetics:
 A:Gene: fimZ
 C:Superfamily: gonococcal fimbril protein
 C:Keywords: fimbria; methylated amino end
 F:1-6/Domain: propeptide #status predicted <PRO>
 F:7-159/Product: fimbril protein fimZ #status predicted <MAT>
 F:7/Modified site: methylated amino end (Phe) (in mature form) #status predicted

Query Match 45.6%; Score 298.5; DB 1; Length 159;
 Best Local Similarity 47.5%; Pred. No. 8.2e-20;
 Matches 56; Conservative 21; Mismatches 40; Indels 1; Gaps 1;
 QY 9 SRSQVRYVAEAGSLKTAVEACLDGRTAVGTAAAGCCDPGATGSSLLTGASQTSQ-TLPTN 67
 DB 36 RSOQVRYVAEAGSLKTAVEACLDGRTAVGTAAAGCCDPGATGSSLLTGASQTSQ-TLPTN 67
 QY 68 TGVPOVDPLTTQTITATFGNGASAAISGQTLTWTRDVGNGMSCATTVDKFPNQC 125
 DB 96 TGVPOVDPLTTQTITATFGNGASAAISGQTLTWTRDVGNGMSCATTVDKFPNQC 153

RESULT 3
 S15266
 fimA protein - Dichelobacter nodosus
 C:Species: Dichelobacter nodosus
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 26-Aug-1999
 C:Accession: S15266
 R:Matlick, J.S.; Anderson, B.J.; Cox, P.T.; Dalrymple, B.P.; Bills, M.M.; Hobbs, M.; Ege
 Mol. Microbiol. 5, 561-573, 1991
 A:Title: Gene sequences and comparison of the fimbril subunits representative of Bacter
 A:Reference number: S15258; MUID:91260440
 A:Accession: S15266
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-156 <MAT>
 A:Cross-references: EMBL:X52389; NID:g39696; PIDN:CAA3618.1; PID:g39697
 C:Superfamily: gonococcal fimbril protein
 C:Keywords: methylated amino end
 F:8/Modified site: methylated amino end (Phe) (in mature form) #status predicted

Query Match 41.9%; Score 274; DB 2; Length 156;
 Best Local Similarity 47.2%; Pred. No. 1.2e-17;
 Matches 59; Conservative 18; Mismatches 38; Indels 10; Gaps 3;
 QY 8 SRSQVRYVAEAGSLKTAVEACLDGRTAVGTAAAGCCDPGATGSSLLTGASQTSQ-TLPTN 64
 DB 36 ARSOVRYVAEAGSLKTAVEACLDGRTAVGTAAAGCCDPGATGSSLLTGASQTSQ-TLPTN 64
 QY 65 PNTGVPVLDPLTT--QTITATFGNGASAAISGQTLTWTRDVGNGMSCATTVDKFPN 122
 DB 91 ATGQAGITITKYPVADDEGNIVATFGNMAAIKPTQTLWRSKRGCTWCATTVDKFPN 150
 QY 123 NGCTD 127
 DB 151 TGCKD 155

RESULT 4
 A46566
 pilin precursor - Dichelobacter nodosus (strain 340, serogroup D)
 C:Species: Dichelobacter nodosus
 C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 26-Aug-1999
 C:Accession: A46566
 R:Finney, K.G.; Elleman, T.C.; Stewart, D.J.
 J. Gen. Microbiol. 134, 575-584, 1988
 A:Title: Nucleotide sequence of the pilin gene of Bacteroides nodosus 340 (serogroup D)
 A:Reference number: A46566; MUID:89036113
 A:Accession: A46566
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-157 <FIN>

A:Cross-references: GB:M20369; NID:g145064; PIDN:AAA23347.1; PID:g145065
 C:Superfamily: gonococcal fimbril protein
 C:Keywords: methylated amino end
 F:8/Modified site: methylated amino end (Phe) (in mature form) #status predicted

Query Match 41.3%; Score 270; DB 2; Length 157;
 Best Local Similarity 45.3%; Pred. No. 2.8e-17;
 Matches 58; Conservative 21; Mismatches 33; Indels 16; Gaps 4;
 QY 8 SRSQVRYVAEAGSLKTAVEACLDGRTAVGTAAAGCCDPGATGSSLLTGASQTSQ-TLPTN 63
 DB 36 ARSOVRYVAEAGSLKTAVEACLDGRTAVGTAAAGCCDPGATGSSLLTGASQTSQ-TLPTN 63
 QY 64 LPNTGV---POVDPLTTQTITATFGNGASAAISGQTLTWTRDVGNGMSCATTVDK 119
 DB 91 ATGQAGITITKYPVADDEGNIVATFGNMAAIKPTQTLWRSKRGCTWCATTVDK 147
 QY 120 RPNCTD 127
 DB 148 RPTGCKD 155

RESULT 5
 A37167
 pilin precursor - Dichelobacter nodosus (strain 351)
 C:Species: Dichelobacter nodosus
 C:Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 26-Aug-1999
 C:Accession: A37167
 R:Hoyle, P.A.; Elleman, T.C.; McKern, N.M.; Stewart, D.J.
 J. Gen. Microbiol. 135, 1113-1122, 1989
 A:Title: Sequence of pilin from Bacteroides nodosus 351 (serogroup H) and implicatio
 A:Reference number: A37167; MUID:90155189
 A:Accession: A37167
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-160 <HOY>
 A:Cross-references: GB:M26980; NID:g145042; PIDN:AAA23336.1; PID:g145043
 C:Superfamily: gonococcal fimbril protein
 C:Keywords: methylated amino end
 F:8/Modified site: methylated amino end (Phe) (in mature form) #status predicted

Query Match 36.5%; Score 239; DB 2; Length 160;
 Best Local Similarity 43.3%; Pred. No. 1.7e-14;
 Matches 55; Conservative 17; Mismatches 43; Indels 12; Gaps 4;
 QY 8 SRSQVRYVAEAGSLKTAVEACLDGRTAVGTAAAGCCDPGATGSSLLTGASQTSQ-TLPTN 67
 DB 36 ARSOVRYVAEAGSLKTAVEACLDGRTAVGTAAAGCCDPGATGSSLLTGASQTSQ-TLPTN 67
 QY 68 TGVPOVDPLTTQTITATFGNGASAAISGQTLTWTRDVGNGMSCATTVDKFPN 120
 DB 91 ADHFGGGLVLDYKLADATNATATFGNMAAIKPTQTLWRSKRGCTWCATTVDKFPN 150
 QY 121 RPNCTD 127
 DB 151 RPTGCKD 157

RESULT 6
 S15267
 fimA protein - Dichelobacter nodosus
 C:Species: Dichelobacter nodosus
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 26-Aug-1999
 C:Accession: S15267
 R:Matlick, J.S.; Anderson, B.J.; Cox, P.T.; Dalrymple, B.P.; Bills, M.M.; Hobbs, M.;
 Mol. Microbiol. 5, 561-573, 1991
 A:Title: Gene sequences and comparison of the fimbril subunits representative of Ba
 A:Reference number: S15258; MUID:91260440
 A:Accession: S15267
 A:Status: preliminary
 A:Molecule type: DNA

A:Residues: 1-156 <MAT>
A:Cross-references: EMBL:X52390; NID:g39703; PIDN:CAA3619.1; PID:g39704
C:Superfamily: gonococcal fimbrial protein
C:Keywords: methylated amino end
F:8/Modified site: methylated amino end (Phe) (in mature form) #status predicted

Query Match 35.6%; Score 232.5; DB 2; Length 156;
Best Local Similarity 40.8%; Pred. No. 6.3e-14;
Matches 53; Conservative 16; Mismatches 38; Indels 23; Gaps 4;

OY 8 SRSQVSRVAAEAGSLKTAVEACLDGRTAVGTAAGCCDPGATGSSLLTGASQTSQTLPTN 67
DB 36 ARSQVSRVAAEAGSLKTAVEACLDGRTAVGTAAGCCDPGATGSSLLTGASQTSQTLPTN 86
OY 68 TGVPOVLPD-----LTQTITIAFGNGASAAISQGLTWTRDVNGWSCATY 115
DB 87 NATAE--DPGCGGLNITVALGSTAENKTEAFPGNAATAHLGKLTWTRSPATWSCSTD 144
OY 116 VDAKFRPNCG 125
DB 145 VDEKFRPNCG 154

RESULT 7

MA7699
Type 4 pilin - Elkenella corrodens
N:Alternate names: N-methylphenylalanine-type pilin
C:Species: Elkenella corrodens
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 26-Aug-1999
C:Accession: A47699; S23844
R:Rao, V.K.; Progulski-Fox, A.
J:Gen. Microbiol. 139, 651-660, 1993
A:Title: Cloning and sequencing of two type 4 (N-methylphenylalanine) pilin genes from B
A:Reference number: A47699; MUID:93232782
A:Accession: A47699
A:Molecule type: DNA
A:Residues: 1-159 <RAO>
A:Cross-references: EMBL:Z12609; NID:g41329; PIDN:CAA78250.1; PID:g41330
A:Experimental source: ATCC 23854
A:Note: sequence extracted from NCBI backbone (NCBIP:130001)
C:Genetics:
A:Gene: ecpa
C:Superfamily: gonococcal fimbrial protein
C:Keywords: methylated amino end
F:8/Modified site: methylated amino end (Phe) (in mature form) #status predicted

Query Match 24.4%; Score 159.5; DB 2; Length 159;
Best Local Similarity 33.1%; Pred. No. 2.2e-07;
Matches 45; Conservative 15; Mismatches 45; Indels 31; Gaps 4;

OY 8 SRSQVSRVAAEAGSLKTAVEACLDGRTAVGTAAGCCDPGAT-----GSSLLT 55
DB 36 SRSQVSRVAAEAGSLKTAVEACLDGRTAVGTAAGCCDPGAT-----GSSLLT 55
OY 56 GASQTSQTLPTNITGVPOVLPDITQTITIAFGNGASAAISQGLTWTRDVNGWSC--- 112
DB 96 AATLTP---GANAG-----DVTEVGLGENANSSIHGATITTLTCTAGSEWTCAVA 142
OY 113 ---ATTVDKFRPNCG 125
DB 143 AGTATGKTKRFPVSGC 158

RESULT 8

A24434
beta fimbrial protein precursor - Moraxella bovis
N:Alternate names: beta pilin
C:Species: Moraxella bovis
C:Date: 08-Aug-1987 #sequence_revision 08-Aug-1987 #text_change 26-Aug-1999
C:Accession: A24434; J10072
R:Marrs, C.F.; Schoolnik, G.; Koomey, J.M.; Hardy, J.; Rothbard, J.; Falkow, S.

J: Bacteriol. 163, 132-139, 1985
A:Reference number: A24434; MUID:85234350
A:Accession: A24434
A:Molecule type: DNA
A:Residues: 1-157 <MAR>
A:Cross-references: GB:M11435; NID:g149760; PIDN:AAA25304.1; PID:g149761
R:Ruehl, W.W.; Marrs, C.F.; Fernandez, R.; Falkow, S.; Schoolnik, G.K.
J:Exp. Med. 168, 983-1002, 1988
A:Title: Purification, characterization, and pathogenicity of Moraxella bovis pil.
A:Reference number: J10071; MUID:89010522
A:Accession: J10072
A:Molecule type: protein
A:Residues: 7-86, 93-122 <RUE>
A:Note: about 50% of the amino-terminus is N-methylated; the remaining 50% of the mo
C:Superfamily: gonococcal fimbrial protein
C:Keywords: methylated amino end; surface antigen
F:1-6/Domain: propeptide #status predicted <PRO>
F:7-157/Product: beta fimbrial protein 1 #status experimental <MAT>
F:8-157/Product: beta fimbrial protein 2 #status experimental <MA2>
F:7/Modified site: methylated amino end (Phe) (in mature form) #status experimental
F:136-155/Disulfide bonds: #status experimental

Query Match 23.5%; Score 153.5; DB 2; Length 157;
Best Local Similarity 31.1%; Pred. No. 7.3e-07;
Matches 42; Conservative 20; Mismatches 46; Indels 27; Gaps 4;

OY 8 SRSQVSRVAAEAGSLKTAVEACLDGRTAVGTAAGCCDP-----GATGSSLLTGAS 58
DB 35 SRSQVSRVAAEAGSLKTAVEACLDGRTAVGTAAGCCDP-----GATGSSLLTGAS 94
OY 59 QTSQTLPTNITGVPOVLPDITQTITIAFGNGASAAISQGLTWTRDVNGWSCATYDA 118
DB 95 ICGAFATCGA-----TLEATIGNRANKDIAGAVITQSRDAGVWTCITNGSA 142
OY 119 -----KFRPNCGTD 127
DB 143 AFGWKSKEVPTCKE 157

RESULT 9

AA2460
fimbrial protein Q - Moraxella lacunata (ATCC 17956) plasmid pMx11
C:Species: Moraxella lacunata
C:Date: 24-Jul-1992 #sequence_revision 24-Jul-1992 #text_change 29-Jan-1999
C:Accession: AA2460
R:Roza, F.W.; Marrs, C.F.
J: Bacteriol. 173, 4000-4006, 1991
A:Title: Interesting sequence differences between the pilin gene inversion regions o
A:Reference number: A42460; MUID:91286182
A:Accession: A42460
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-164 <ROZ>
A:Cross-references: GB:M59711
C:Genetics:
A:Genome: plasmid
C:Superfamily: gonococcal fimbrial protein
C:Keywords: methylated amino end
F:7/Modified site: methylated amino end (Phe) (in mature form) #status predicted

Query Match 23.5%; Score 153.5; DB 2; Length 164;
Best Local Similarity 35.9%; Pred. No. 7.7e-07;
Matches 47; Conservative 15; Mismatches 54; Indels 15; Gaps 4;

OY 8 SRSQVSRVAAEAGSLKTAVEACLDGRTAV-----GTAAGCCDPGATGSSLLTGASQTSQ 63
DB 35 SRSQVSRVAAEAGSLKTAVEACLDGRTAV-----GTAAGCCDPGATGSSLLTGASQTSQ 90
OY 64 LPTNITGVPOV-LDPLTQTITIAFGNGASAAISQGLTWTRDVNGWSC-----ATTV 116
DB 116 LPTNITGVPOV-LDPLTQTITIAFGNGASAAISQGLTWTRDVNGWSC-----ATTV 116

Db 91 LKETGGVYIAGFSATSSAGTTTGLGNRANKDISGALITOKRANGVWTHVQGTATGW 150
 QY 117 DAKFRPNCCTD 127
 Db 151 KDKFIPCTGCTN 161

RESULT 10
 S04440
 fimbrial protein - Pseudomonas aeruginosa (strain 1244)
 N:Alternate names: pilin
 C:Species: Pseudomonas aeruginosa
 C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 26-Aug-1999
 C:Accession: S04440
 R:Castic, P.A.; Siderbery, H.F.; Sadoff, J.C.
 Mol. Gen. Genet. 216, 75-80, 1989
 A:Title: Cloning and sequencing of the Pseudomonas aeruginosa 1244 pilin structural gene
 A:Reference number: S04440; MUID:89281493
 A:Accession: S04440
 A:Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-154 <CAS>
 C:Superfamily: gonococcal fimbrial protein

Query Match 23.2%; Score 151.5; DB 2; Length 154;
 Best Local Similarity 31.7%; Pred. No. 1,1e-06;
 Matches 38; Conservative 25; Mismatches 44; Indels 13; Gaps 3;

QY 8 SRSQVSRVMAEAGSLKTAVEACLODGRVAGTAA---GCCDPGATGSSLLTGASQTSQTL 64
 Db 35 ARQVTRVAVSEVSAKTAIAESALIEGKEIVSSATPKDYDIDGFTESTLIDSGSKSQ--- 91
 QY 65 PTNTGVPQVLDPLTTQTIIATFGNGASAAISGOTLTMTFVDVNGWSC-ATTVDAKFRPN 123
 Db 92 -----IQVTDNDQDGTVELVATLKGSSGSAIKGAVTVSRKNDGVWCKITPTPAWKP 145

RESULT 11
 B31105
 fimbrial protein precursor - Pseudomonas aeruginosa (strain P1)
 C:Species: Pseudomonas aeruginosa
 C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 08-Oct-1999
 R:Pasloske, B.L.; Sastriy, P.A.; Finlay, B.B.; Paranchych, W.
 J. Bacteriol. 170, 3738-3741, 1988
 A:Title: Two unusual pilin sequences from different isolates of Pseudomonas aeruginosa.
 A:Reference number: A91879; MUID:88298689
 A:Accession: B31105
 A:Molecule type: DNA
 A:Residues: 1-154 <PAS>
 A:Cross-references: GB:M21652; NID:g151471; PIDN:AMC63060.1; PID:g151472
 C:Superfamily: gonococcal fimbrial protein
 F:1-6/Domain: signal sequence #status predicted <STS>
 F:7-154/Product: fimbrial protein #status predicted <MAT>

Query Match 23.2%; Score 151.5; DB 2; Length 154;
 Best Local Similarity 31.7%; Pred. No. 1,1e-06;
 Matches 38; Conservative 25; Mismatches 44; Indels 13; Gaps 3;

QY 8 SRSQVSRVMAEAGSLKTAVEACLODGRVAGTAA---GCCDPGATGSSLLTGASQTSQTL 64
 Db 35 ARQVTRVAVSEVSAKTAIAESALIEGKEIVSSATPKDYDIDGFTESTLIDSGSKSQ--- 91
 QY 65 PTNTGVPQVLDPLTTQTIIATFGNGASAAISGOTLTMTFVDVNGWSC-ATTVDAKFRPN 123
 Db 92 -----IQVTDNDQDGTVELVATLKGSSGSAIKGAVTVSRKNDGVWCKITPTPAWKP 145

RESULT 12
 A41490
 pilin precursor - Moraxella bovis

C:Species: Moraxella bovis
 C:Date: 10-Apr-1992 #sequence_revision 10-Apr-1992 #text_change 26-Aug-1999
 C:Accession: A41490
 R:Elleman, T.C.; Hoyne, P.A.; Lepper, A.W.D.
 Infect. Immun. 58, 1678-1684, 1990
 A:Title: Characterization of the pilin gene of Moraxella bovis Dalton 2d and express
 A:Reference number: A41490; MUID:90256243
 A:Accession: A41490
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-156 <ELI>
 A:Cross-references: GB:M2155; GB:M2665; NID:g149758; PIDN:AAA53087.1; PID:g149759
 C:Superfamily: gonococcal fimbrial protein
 C:Keywords: methylated amino end
 F:7/Modified site: methylated amino end (Phe) (in mature form) #status predicted

Query Match 21.8%; Score 142.5; DB 2; Length 156;
 Best Local Similarity 30.2%; Pred. No. 7e-06;
 Matches 42; Conservative 15; Mismatches 43; Indels 39; Gaps 4;

QY 8 SRSQVSRVMAEAGSLKTAVEACLODGRVAGTAA---GCCDPGATGSSLLTGASQTSQTL 64
 Db 35 SKSQTTRVVGELAAAKTGADALFEKTPV-----VNSADGIAEVDIGIGEAATPRSN 88
 QY 53 LITGASQTSQTLPTNTGVPQVLDPLTTQTIIATFGNGASAAISGOTLTMTFVDVNGWSC 112
 Db 89 LLSAVSFTFTKGSN-----GTISGTIGCANNDIRGTVISQERDGTGWSG 135
 QY 113 ATTVA-----KERNGCT 126
 Db 136 KVTGNGTGMKDKFPTGCT 154

RESULT 13
 J10071
 alpha-pilin - Moraxella bovis (strain Epp63)
 C:Species: Moraxella bovis
 A:Note: host Bos primigenius taurus (cattle)
 C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 08-Nov-1996
 C:Accession: J10071
 R:Ruehl, W.W.; Marrs, C.F.; Fernandez, R.; Falkow, S.; Schoolnik, G.K.
 J. Exp. Med. 168, 983-1002, 1988
 A:Title: Purification, characterization, and pathogenicity of Moraxella bovis pilin.
 A:Reference number: J10071; MUID:89010522
 A:Accession: J10071
 A:Molecule type: protein
 A:Residues: 1-155 <RUE>
 A:Note: about 50% of the amino-terminus is N-methylated; the remaining 50% of the mo
 C:Superfamily: gonococcal fimbrial protein
 C:Keywords: methylated amino end
 F:1-155/Product: alpha-pilin 1 #status experimental <MAT>
 F:2-155/Product: alpha-pilin 2 #status experimental <MAT>
 F:1/Modified site: methylated amino end (Phe) #status experimental
 F:131-150/Disulfide bonds: #status experimental

Query Match 19.7%; Score 129; DB 2; Length 155;
 Best Local Similarity 31.8%; Pred. No. 0.00011;
 Matches 41; Conservative 17; Mismatches 53; Indels 18; Gaps 4;

QY 8 SRSQVSRVMAEAGSLKTAVEACLODGRVAGTAA---GCCDPGATGSSLLTGASQTSQTLPTN 67
 Db 29 SKSQTTRVVGELAAKTGADALFEKTPV-----LSESSVSKENIGLTSSTTRKPS 83
 QY 68 TGVPOVLDPLT-----TQTIIATFGNGASAAISGOTLTMTFVDVNGWSC-----ATTV 116
 Db 84 NIMASY--ELTGRADGAGTISATLGNKANKDIATVITQERTTGDVWTKIDGSOAAKY 141
 QY 117 DAKFRPNC 125
 Db 142 KEKFNPTGC 150

RESULT 14
S52693
fimbriillin - Xanthomonas campestris
C:Species: Xanthomonas campestris
C>Date: 19-May-1995 #sequence_revision 01-Sep-1995 #text_change 24-Nov-1999
C:Accession: S52693
R:Ojaneen, T.M.; Kalkkinen, N.; Westerlund, B.; van Doorn, J.; Hahtela, K.; Korhonen, T.
submitted to the EMBL Data Library, March 1995
A:Description: Characterization of the fimA gene encoding the type IV fimbriillin of the
A:Reference number: S52692
A:Accession: S52693
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-135 <OJA>
A:Cross-references: EMBL:Z48759; NID:9747907; PIDN:CAA88681.1; PID:9747909
C:Superfamily: gonococcal fimbrial protein

Query Match 19.6%; Score 128.5; DB 2; Length 135;
Best Local Similarity 31.9%; Pred. No. 0.00011;
Matches 38; Conservative 18; Mismatches 44; Indels 19; Gaps 5;

OY 8 SRSQVSRVMAEAGSLKTVEACLDGRTAVGTAGCCDPGATGSSLLTGASQTSQTLPTN 67
DB 35 AKAOITLALAEIRPKGTTEAAVOD---GTNPSVIDAPYIGLSTRCARVSAVL-SS 88
OY 68 TGVPOVLDPITTTQTTIATFGNGASAAISGOTLTWTRDNGWGC-ATTVDKFRPNC 125
DB 89 TGVAEI--SCLQ-----GSALVSGMDLKLRASADGWCIDGSAPDAKFRPAC 135

RESULT 15
A55851
prepilin - Moraxella bovis
C:Species: Moraxella bovis
C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 26-Aug-1999
C:Accession: A55851
R:Atwell, J.L.; Tennent, J.M.; Lepper, A.W.; Eilerman, T.C.
J. Bacteriol. 176, 4875-4882, 1994
A:Title: Characterization of pilin genes from seven serologically defined prototype strains
A:Reference number: A55851; MUID:94327452
A:Accession: A55851
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-158 <RES>
A:Cross-references: GB:L32965; NID:948303; PIDN:AAA53558.1; PID:948304
C:Superfamily: gonococcal fimbrial protein
C:Keywords: methylated amino end
F:7/Modified site: methylated amino end (Phe) (in mature form) #status predicted

Query Match 19.0%; Score 124.5; DB 2; Length 158;
Best Local Similarity 31.6%; Pred. No. 0.00029;
Matches 43; Conservative 16; Mismatches 46; Indels 31; Gaps 5;

OY 8 SRSQVSRVMAEAGSLKTVEACLDGRTAV-CTAAGCCDPGATGSSLLTGASQTSQTLPT 66
DB 35 SKSQTRVVGELAAAGTAVDAALFEGKTPVLGTT-----TTTKEDIGLTT 80
OY 67 NTGVPO-----VLDP---LTTQTTIATFGNGASAAISGOTLTWTRDNGWGC----- 112
DB 81 AGGTPRSNLVSAVTLDDGAFATGEGSIKAVLGTFRANKDIAGAEIKQIRNDGQWGCVEKA 140
OY 113 --ATTVDKFRPNCCT 126
DB 141 AGAPGFKDKFTPTGCT 156

Search completed: February 8, 2002, 15:25:57
Job time: 162 sec

Fri Feb 8 15:44:48 2002

us-09-865-159-10.rpr

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 8, 2002, 15:34:23 ; Search time 22.14 Seconds

(Without alignments)
210.318 Million cell updates/sec

Title: US-09-865-159-10

Perfect score: 654
Sequence: 1 ALBGTFFSRSOVSRYMAEAG.....GGWSCATYDAKPRPGCTD 127

Scoring table: BLOSUM62
Gapop 10.0 ; Gapext 0.5

Searched: 100059 segs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	305.5	46.7	159	1	FMZD_BACNO
2	298.5	45.6	159	1	FMZD_BACNO
3	274	41.9	156	1	FMAD_BACNO
4	239	36.5	160	1	FMAD_BACNO
5	233.5	36.0	156	1	FMAD_BACNO
6	159.5	24.4	159	1	ECPA_EIKCO
7	153.5	23.5	157	1	FMQ_MORBO
8	151.5	23.2	154	1	FM12_PSEAE
9	151.5	23.2	154	1	FMK1_PSEAE
10	135	20.6	23	1	FMK7_PSEAE
11	129	19.7	159	1	FM1_MORBO
12	117.5	18.0	150	1	FM3_PSEAE
13	115.5	17.7	136	1	FMQC_PSEAE
14	115.5	17.7	150	1	FMQC_PSEAE
15	112	17.1	150	1	FMQA_PSEAE
16	108	16.5	159	1	ECPB_EIKCO
17	107.5	16.4	149	1	FMPO_PSEAE
18	97.5	14.9	153	1	ECPC_EIKCO
19	90	13.8	515	1	GUND_CLOCL
20	89	13.6	161	1	FMAG_BACNO
21	89	13.6	162	1	FMAG_BACNO
22	88	13.5	157	1	FMPL_PSEAE
23	87.5	13.4	160	1	FMAB_BACNO
24	87	13.3	471	1	GUX2_TRIE
25	84	12.8	161	1	FMAT_BACNO
26	83	12.7	449	1	GUNA_CELFI
27	82.5	12.6	142	1	TAPA_AERYH
28	82	12.5	161	1	FMAX_BACNO
29	81.5	12.5	484	1	GUX_CELFI
30	81.5	12.4	1569	1	YPOA_ECOLI
31	81	12.4	154	1	FMW_MORNO
32	81	12.4	293	1	PRTT_TRIAL
33	80.5	12.3	158	1	FMAF_BACNO

34	80.5	12.3	160	1	FMAT_BACNO	P27691 bacterioides
35	79	12.1	610	1	POQC_BRARE	P31367 brachydanio
36	78.5	12.0	161	1	FMAT_BACNO	P27689 bacterioides
37	78	11.9	1120	1	STFR_ECOLI	P76072 escherichia
38	77.5	11.9	160	1	FMAT_BACNO	P27690 bacterioides
39	77.5	11.9	264	1	MSA2_PLAF	P19599 plasmodium
40	76.5	11.7	532	1	SP67_DICDI	P22698 dictyostell
41	76.5	11.7	693	1	CAUP_DROME	P54269 dirosophila
42	76	11.6	264	1	MSA2_PLAF	P50499 plasmodium
43	76	11.6	563	1	MUCS_BOVIN	P98091 bos taurus
44	75.5	11.5	329	1	YK23_YEAST	P36110 saccharomyc
45	74.5	11.4	160	1	FMAT_BACNO	P27688 bacterioides

ALIGNMENTS

```

RESULT 1
FMZD_BACNO STANDARD; PRT; 159 AA.
ID FMZD_BACNO
AC P17416;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE POSSIBLE MINOR FIMBRIAL PROTEIN PRECURSOR (PILIN) (SEROGROUP D).
GN FIMZ.
OS Bacterioides nodosus (Dichelobacter nodosus).
OC Bacteria; Proteobacteria; gamma subdivision; Cardiobacteriaceae;
OC Dichelobacter.
OX NCBI_TaxID=870;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SEROGROUP D ISOLATE VCS1172;
RX MEDLINE=91260439; PubMed=1675418;
RA Hobbs M., Dalrymple B.P., Cox P.T., Livingstone S.P., Delaney S.F.,
RA Mattick J.S.;
RT "Organization of the fimbrial gene region of Bacterioides nodosus:
RT class I and class II strains."
RT Mol. Microbiol. 5:543-560(1991).
RL -I- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.
CC -I- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
CC
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC
CC EMBL: X52389; NOT_ANNOTATED_CDS.
CC PIR: S15249; YOBBDZ.
DR HSSP: P02974; IATZ.
DR InterPro: IPR001082; Pilin.
DR InterPro: IPR001120; Prok_N_methyltn.
DR Pfam: PF00114; pilin; 1.
DR ProDom: PD000666; pilin; 1.
DR PROSITE: PS000409; PROKAR_NTER_METHYL; 1.
KW Fimbria; Methylation.
FT PROPEP 1
FT CHAIN 7
FT MOD_RES 7 159 POSSIBLE MINOR FIMBRIAL PROTEIN.
FT DISULFID 56 71 METHYLATION (BY SIMILARITY).
FT DISULFID 140 153 BY SIMILARITY.
SQ SEQUENCE 159 AA; 17102 MW; E53B0BC52B808C2 CRC64;

```

Query Match 46.7%; Score 305.5; DB 1; Length 159;
Best Local Similarity 49.2%; Pred. No. 2.6e-21;
Matches 58; Conservative 20; Mismatches 39; Indels 1; Gaps 1;

OY 9 RSOVSRYVAEAGSLKTAVEACLODGRVAVTAAGCCPGATGSSLLTGAQTSQ-TLPTN 67
 DB 36 RSOVTRVLAEGELRLAVAOCLNDGTTTVGANGNECDPRASGNSITSGANDEIYIAN 95
 OY 68 TGVPOVLDPLTQTITIAFGNGASAAISGQTLTWTRDVNGSCATYADAKFRPNC 125
 DB 96 TGVQFPNPLTEETALTATFNNSAASIIHGKLIWROKSGSWYCHSNAEKFLPSGC 153

RESULT 2
 FMZH_BACNO STANDARD: PRT; 159 AA.
 AC P17417;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE POSSIBLE MINOR FIMBRIAL PROTEIN PRECURSOR (PILIN) (SEROGROUP H1).
 GN FIM2.
 OS Bacteroides nodosus (Dichelobacter nodosus).
 CC Bacteria; Proteobacteria; gamma subdivision; Cardiobacteriaceae;
 CC Dichelobacter.
 OX NCBI_Taxid=870;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SEROGROUP H1 ISOLATE VCS1215;
 RX MEDLINE=91260439; PubMed=1675418;
 RA Hobbs M., Dalrymple B.P., Cox P.T., Livingstone S.P., Delaney S.F.,
 Mattick J.S.;
 RT "Organization of the fimbrial gene region of Bacteroides nodosus:
 class I and class II strains.";
 RL Mol. Microbiol. 5:543-560(1991).
 CC -1- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
 NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
 CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
 CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.
 CC -1- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC
 CC -----
 DR EMBL; X52390; CAA36622.1; -
 DR PIR; S15251; Y0B2H2.
 DR HSSP; P02974; IAY2.
 DR InterPro; IPR001082; PiliN.
 DR InterPro; IPR001120; Prok_N_methyltn.
 DR Pfam; PF00114; piliN; 1.
 DR ProDom; PD000666; PiliN; 1.
 DR PROSITE; PS00409; PROKAR_NTER_METHYL; 1.
 KW Fimbria; Methylation.
 FT PROPEP 1 6
 FT CHAIN 7 159 POSSIBLE MINOR FIMBRIAL PROTEIN.
 FT MOD_RES 7 7 METHYLATION (BY SIMILARITY).
 FT DISULFID 56 71 BY SIMILARITY.
 FT DISULFID 140 153 BY SIMILARITY.
 FT DISULFID 159 AA; 1718 MW; 7D928B7E0A8BDC5 CRC64;
 SQ SEQUENCE

Query Match 45.6%; Score 298.5; DB 1; Length 159;
 Best Local Similarity 47.5%; Pred. No. 1.1e-20; Mismatches 40; Indels 1; Gaps 1;
 Matches 56; Conservative 21; Mismatches 40; Indels 1; Gaps 1;

OY 9 RSOVSRYVAEAGSLKTAVEACLODGRVAVTAAGCCPGATGSSLLTGAQTSQ-TLPTN 67
 DB 36 RSOVTRVLAEGELRLAVAOCLNDGTTTVGANGNECDPRASGNSITSGANDEIYIAN 95
 OY 68 TGVPOVLDPLTQTITIAFGNGASAAISGQTLTWTRDVNGSCATYADAKFRPNC 125
 DB 96 TGVQFPNPLTEETALTATFNNSAASIIHGKLIWROKSGSWYCHSNAEKFLPSGC 153

DB 96 TGVQFPNPLTEETALTATFNNSAASIIHGKLIWROKSGSWYCHSNAEKFLPSGC 153

RESULT 3
 FMZH_BACNO STANDARD: PRT; 156 AA.
 AC P13253;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE FIMBRIAL PROTEIN PRECURSOR (PILIN) (SEROGROUP D) (340 ANTIGEN).
 GN FIMA.
 OS Bacteroides nodosus (Dichelobacter nodosus).
 CC Bacteria; Proteobacteria; gamma subdivision; Cardiobacteriaceae;
 CC Dichelobacter.
 OX NCBI_Taxid=870;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SEROGROUP D ISOLATE VCS1172;
 RX MEDLINE=91260440; PubMed=1675419;
 RA Mattick J.S., Anderson B.J., Cox P.T., Dalrymple B.P., Bills M.M.,
 Hobbs M., Egerton J.R.;
 RT "Gene sequences and comparison of the fimbrial subunits
 representative of Bacteroides nodosus serotypes A to I: class I and
 class II strains.";
 RL Mol. Microbiol. 5:561-573(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SEROGROUP D ISOLATE 340;
 RX MEDLINE=89036113; PubMed=3183618;
 RA Finney K.G., Ellemann T.C., Stewart D.J.;
 RT "Nucleotide sequence of the pilin gene of Bacteroides nodosus 340
 (serogroup D) and implications for the relatedness of serogroups.";
 RL J. Gen. Microbiol. 134:575-584(1988).
 CC -1- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
 NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
 CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
 CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.
 CC -1- MISCELLANEOUS: THE SEQUENCE SHOWN IS THAT OF ISOLATE 340.
 CC -1- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC
 CC -----
 DR EMBL; X52389; CAA36618.1; -
 DR EMBL; M20369; AAA23347.1; -
 DR PIR; S15266; S15266.
 DR HSSP; Q53391; IKB8.
 DR InterPro; IPR001082; PiliN.
 DR InterPro; IPR001120; Prok_N_methyltn.
 DR Pfam; PF00114; piliN; 1.
 DR ProDom; PD000666; PiliN; 1.
 DR PROSITE; PS00409; PROKAR_NTER_METHYL; 1.
 KW Fimbria; Methylation.
 FT PROPEP 1 7
 FT CHAIN 8 156 FIMBRIAL PROTEIN.
 FT MOD_RES 8 8 METHYLATION (BY SIMILARITY).
 FT DISULFID 57 67 BY SIMILARITY.
 FT DISULFID 140 153 BY SIMILARITY.
 FT VARIANT 65 66 GE -> DK (IN ISOLATE 340).
 FT VARIANT 80 80 D -> E (IN ISOLATE 340).
 FT VARIANT 95 95 A -> T (IN ISOLATE 340).
 SQ SEQUENCE 156 AA; 16544 MW; 45418C8C22BB93C CRC64;

Query Match 41.9%; Score 274; DB 1; Length 156;
 Best Local Similarity 47.2%; Pred. No. 1.9e-18; Mismatches 38; Indels 10; Gaps 3;
 Matches 59; Conservative 18; Mismatches 38; Indels 10; Gaps 3;


```

OY      8 SRSOVSRYMAAGSLKTAVEACLDGRTAVGTAAQCQDPGANGSSLLTNG---ASQTSOTL 64
        | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db      36 ARSOVSRYMSETGQRRATLFTCVLDGK-----EAGECHTGTGSLTLDGDTTAGESTAA 90
        | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
OY      65 PTNNGVPOVDELPLTT--OTTTIATFGNGASAAISGOTLTWTRDVGNGSCATTVDAKFRP 122
        | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db      91 ATGQAGITIKFPAVAADDEGNIVATFGRNAANAIRPQTLTFRSRSKGTCTCATFTYEAQRK 150
        | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
OY      123 NGCMD 127
        || |
Db      151 TGCKD 155

RESULT      4
FMAJ_BACNO  ID FMAJ_BACNO      STANDARD:      PRT:      160 AA.
AC      PI9528
DT      01-FEB-1991 (Rel. 17, 'Created)
DT      01-FEB-1991 (Rel. 17, 'Last sequence update)
DT      01-FEB-1991 (Rel. 17, 'Last annotation update)
DE      FIMBRIAL PROTEIN PRECURSOR (PILIN) (SEROGRUOP H) (351 ANTIGEN).
GN      FIMA.
OS      Bacteroides nodosus (Dichelobacter nodosus).
OC      Bacteria; Proteobacteria; gamma subdivision; Cardiobacteriaceae;
CC      Dichelobacter.
OX      NCBI_Taxid=870;
      [1]
RN      SEQUENCE FROM N.A.
RP      STRAIN=SEROGRUOP H ISOLATE 351;
RC      MEDLINE=90155189; PubMed=2621448;
RX      Hoynes P.A., Elleman T.C., McKern N.M., Stewart D.J.:
RA      "Sequence of pilin from Bacteroides nodosus 351 (Serogroup H) and
RT      implications for serogroup classification.",
      J. Gen. Microbiol. 135:1113-1122(1989).
RL      -1- SUBUNIT: THE PILIN ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
      NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
      CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
      CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.
CC      -1- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; M26980; AAA23386.1; .
DR      PIR; A37167; A37167.
DR      HSSP; O53391; 1KB8.
DR      InterPro; IPR001082; Pilin.
DR      InterPro; IPR001120; ProX_N_Methyltn.
DR      Pfam; PF00114; Pilin; 1.
DR      ProDom; PD000666; Pilin; 1.
DR      ProSITE; PS00409; PROKAR_NTER_METHYL. 1.
KW      Fimbria; Methylation.
FT      PROPEP      1      7
FT      CHAIN      8      160      FIMBRIAL PROTEIN.
FT      MOD_RES      8      8      METHYLATION (BY SIMILARITY).
SQ      SEQUENCE      160 AA; 17169 MW; 3160DAEAFE87ABAA CRC64;

Query Match      36.5%; Score 239; DB 1; Length 160;
Best Local Similarity 43.3%; Pred. No. 3.2e-15;
Matches 55; Conservative 17; Mismatches 43; Indels 12; Gaps 4;

OY      8 SRSOVSRYMAAGSLKTAVEACLDGRTAVGTAAQCQDPGANGSSLLTNGASQTSOTLPTN 67
        | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db      36 ARSOVSRYMSETGQRRATLFTCVLDGK-----KADECFIGWKSNNLGAAGSPSSNDST 90
        | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
OY      68 TGVV---QVLD-PLTTOQT--TITTFGNGASAAISGOTLTWTRDVGNGSCATTVDAKE 120

```

Db	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50
ADHPGCGGLVLDYKLEADATNAITATPFQGNNAATLHGKALWTRDPKATWCSGTVEIKF	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50
121 RPNGCTD 127	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50
151 RPTGCKD 157	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50
RESULT 5	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50
FMH_BACNO	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50
FMH_BACNO	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50
STANDARD:	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50
PRT:	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50
156 AA.	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50
13-AUG-1987 (Rel. 05, Created)	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50
13-AUG-1987 (Rel. 05, Last sequence update)	1	2	3	4	5	6	7	8	9	10	11	12	13	1																																				

```

Db      36 SKSOVTRAYGCMATKTAIEALFECHTSPVLAATAAAGCAATPENWGMHLDNTSNLLS 95
Qy      56 GASQTSQTLPLTNGVPOVLDPLTTQTTLITATFGGASAAISGOTLWTRDVGNGWSC-- 112
Db      96 AATLT-----GANA-----DYTFVGTGLGENANSSIHGATITLTCTAGCWTCAVA 142
Qy      113 ---ATTVDARFRPNCG 125
Db      143 AGTATGKTKTKEPSPSC 158

RESULT 7
FMO MORBO ID FMO MORBO STANDARD: PRT: 157 AA.
AC P07640;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE FIMBRIAL PROTEIN Q PRECURSOR (BETA PILIN) (Q PILIN).
OS Moraxella bovis.
OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae; Moraxella.
OX NCBI_TaxID=476;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EPP63;
RX MEDLINE=85234350; PubMed=2861194;
RA Mairs C.F., Schoolnik G., Koomey J.M., Hardy J., Rothbard J.,
   Falkow S.;
RT "Cloning and sequencing of a Moraxella bovis pilin gene.";
RL J. Bacteriol. 163:132-139(1985).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=EPP63;
RX MEDLINE=90094235; PubMed=2403542;
RA Fuls R.A., Mairs C.F., Stevens S.P., Green M.R.;
RT "Sequence analysis of the inversion region containing the pilin genes
   of Moraxella bovis.";
RL J. Bacteriol. 172:310-316(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=91286182; PubMed=2061282;
RA Roza F.W., Mairs C.F.;
RT "Interesting sequence differences between the pilin gene inversion
   regions of Moraxella leuconata ATCC 17956 and Moraxella bovis Epp63.";
RL J. Bacteriol. 173:4000-4006(1991).
RN [4]
RP SEQUENCE OF 7-157.
RX MEDLINE=89010522; PubMed=2902184;
RA Ruell W.W., Mairs C.F., Fernandez R., Falkow S., Schoolnik G.K.;
RT "Purification, characterization, and pathogenicity of Moraxella bovis
   pilin.";
RL J. Exp. Med. 168:983-1002(1988).
RN [5]
RP SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
   NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
   CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
   CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED FILIUS.
RN [6]
RP MISCELLANEOUS: MORAXELLA BOVIS CAN EXPRESS EITHER A Q OR A I
   PILIN. THE INVERSION OF 2 KB OF DNA DETERMINES WHICH PILIN IS
   EXPRESSED.
RN [7]
RP SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.

-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and that statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL, M11435; AAA25304.1; -
CC EMBL, M32345; AAA88223.1; -
CC EMBL, M59712; AAA25308.1; -

```

```

DR PIR: A24434; A24434.
DR PIR: J10072; J10072.
DR InterPro: IPR001082; Piliin.
DR Pfam: PF00114; Piliin; 1.
DR ProDom: PD000666; Piliin; 1.
DR PROSITE: PS00409; PROKAR_NTER_METHYL. 1.
KW Fimbria; Methylation.
FT PROPEP 1 6
FT CHAIN 7 157 FIMBRIAL PROTEIN Q.
FT MOD_RES 7 7 METHYLATION.
FT DISULFD 136 155 BY SIMILARITY.
SQ SEQUENCE 157 AA: 16006 MW: A923CD8A26C693C9 CRC64:

Query Match 23.5%; Score 153.5; DB 1; Length 157;
Best Local Similarity 31.1%; Pred. No. 2e-07;
Matches 42; Conservative 20; Mismatches 46; Indels 27; Gaps 4;

OY 8 SRSQVSRMAEAGSLKTAVEACLDGRT-ANGTAAGQCDP-----GATGSSLLTGAS 58
Db 35 SKSQTRVAVGELAAKGTAVDAALFEGKTPKLGKANDTEEDIGLTTGGTARSNLMSSVN 94
OY 59 QTSQTLPTNGVPLDPLTQTITIAFGNGASAAISGQTLTWTRDYGNGSCATTVDA 118
Db 95 IGGGAFATGAG-----TLEATLGNRANKDINAGAVITQSRDAEGVWCTINGSA 142
OY 119 -----KFRPNGCTD 127
Db 143 APGWKSKFVPTGCKE 157

RESULT 8
FM12_PSEAE STANDARD: PRT; 154 AA.
AC P18774;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE FIMBRIAL PROTEIN PRECURSOR (PILIIN) (STRAIN 1244).
GN PILA OR FIWA.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89281493; PubMed=2499765;
RA Castrie P.A., Sidberry H.F., Sadoff J.C.;
RT "Cloning and sequencing of the Pseudomonas aeruginosa 1244 piliin
structural gene.";
RL Mol. Gen. Genet. 216:75-80(1989).
CC -1- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
CC NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
CC CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
CC CONFIRMATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.
CC -1- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X83916; CA58768.1; -
DR PIR: S04440; S04440.
DR HSSP: P02974; 1AY2.
DR InterPro: IPR001082; Piliin.
DR InterPro: IPR001120; Prok_N_methyltn.
DR Pfam: PF00114; Piliin; 1.
DR ProDom: PD000666; Piliin; 1.

```

```

DR PROSITE: PS00409; PROKAR_NTER_METHYL. 1.
KW Fimbria; Methylation.
FT PROPEP 1 6
FT CHAIN 7 154 FIMBRIAL PROTEIN.
FT MOD_RES 7 7 METHYLATION (BY SIMILARITY).
FT DISULFD 133 151 BY SIMILARITY.
SQ SEQUENCE 154 AA: 16277 MW: 9A6E09E0A6C66AD0 CRC64:

Query Match 23.2%; Score 151.5; DB 1; Length 154;
Best Local Similarity 31.7%; Pred. No. 3e-07;
Matches 38; Conservative 25; Mismatches 44; Indels 13; Gaps 3;

OY 8 SRSQVSRMAEAGSLKTAVEACLDGRTAVGTA---GCCDPAAGSSLLTGASQTSQTL 64
Db 35 ARTQTVRAVSEVSAALTAESAAILGCKEIVSATPKDQYDIGFTSTLLDGSQSKQ--- 91
OY 65 PINTGVPLDPLTQTITIAFGNGASAAISGQTLTWTRDYGNGMSC-ATTVDKFRPN 123
Db 92 -----IOVTNQDGTVELVATLTKSSGSAIKGAVITVSRKNDGVWNCKITPTPAKPN 145

RESULT 9
FMK1_PSEAE STANDARD: PRT; 154 AA.
AC P17836;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE FIMBRIAL PROTEIN PRECURSOR (PILIIN) (STRAIN K122-4).
GN PILA OR FIWA.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-K122-4;
RA MEDLINE=86298689; PubMed=2841299;
RA Pasloske B.L., Sastry P.A., Finlay B.B., Paranchych W.;
RT "Two unusual piliin sequences from different isolates of Pseudomonas
aeruginosa.";
RL J. Bacteriol. 170:3738-3741(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN-9D2;
RA MEDLINE=94131566; PubMed=7507890;
RA Castrie P.A., Deal C.D.;
RT "Differentiation of Pseudomonas aeruginosa pili based on sequence and
B-cell epitope analyses.";
RL Infect. Immun. 62:371-376(1994).
CC -1- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
CC NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
CC CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
CC CONFIRMATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.
CC -1- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M21652; AAC63060.1; -
DR EMBL: S68100; AAC60460.1; -
DR PIR: B31105; B31105.
DR HSSP: P02974; 1AY2.
DR InterPro: IPR001082; Piliin.
DR InterPro: IPR001120; Prok_N_methyltn.
DR Pfam: PF00114; Piliin; 1.
DR ProDom: PD000666; Piliin; 1.

```

DR PROSITE; PS00409; PROKAR_NTER_METHYL, 1.
 KW Fimbria; Methylation.
 FT PROPEP 1 6
 FT CHAIN 7 154
 FT MOD_RES 7 7 FIBRIAL PROTEIN.
 FT DISULFID 133 151 METHYLATION (BY SIMILARITY).
 FT DISULFID 133 151 BY SIMILARITY.
 SQ SEQUENCE 154 AA; 16278 MW; 807409FABCC6A00 CRC64;

Query Match 23.2%; Score 151.5; DB 1; Length 154;
 Best Local Similarity 31.7%; Pred. No. 3e-07;
 Matches 38; Conservative 25; Mismatches 44; Indels 13; Gaps 3;

QY 8 SRSQSVRYMAEAGSLKTAVEACLDGRTAVGTAA---GQCDPQATGSSLLTGASQTSOTL 64
 DB 35 ARTQYTRAVSEVSLKTAESAILEGKEIVASATPKPTQIDIGTSTLDGSGKSG--- 91
 QY 65 PTNNGVQVLDPTTQTTTITFNGASASISGQTLTWTRDVGNGWSC-ATTVDAKFRPN 123
 DB 92 -----TQVTDNKDGTVELVATLTKSSGSAIKGAVITVSRKNDGVNCKITKPTLAKPN 145

RESULT 10
 FMK7_PSEAE STANDARD; PRT; 23 AA.
 AC 053391;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE FIBRIAL PROTEIN (PILIN) (STRAIN KB7) (FRAGMENT).
 GN PIL.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=KB7;
 RX MEDLINE=94103636; PubMed=7903973;
 RA IPATSG;
 RT "A multicenter comparison of methods for typing strains of
 RT Pseudomonas aeruginosa predominantly from patients with cystic
 RT fibrosis. The International Pseudomonas aeruginosa Typing Study
 RT Group.";
 RL J. Infect. Dis. 169:134-142(1994).
 RN [2]
 RP STRUCTURE BY NMR OF 7-23.
 RC STRAIN=KB7;
 RX MEDLINE=96110702; PubMed=8845350;
 RA Campbell A.P., McInnes C., Hodges R.S., Sykes B.D.;
 RT "Comparison of NMR solution structures of the receptor binding
 RT domains of Pseudomonas aeruginosa pilin strains PMO, KB7, and PAK:
 RT implications for receptor binding and synthetic vaccine design.";
 RL Biochemistry 34:16255-16268(1995).
 CC -1- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
 CC NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH. THEY
 CC CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
 CC CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.
 CC -1- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.

 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DR EMBL; S67809; CAB32861.1;
 DR PDB; 1KB7; 29-JAN-96.
 DR PDB; 1KB8; 29-JAN-96.
 DR InterPro; IPR001082; Pilin.
 DR InterPro; IPR001120; Prok_N_methyltn.

DR Pfam; PF00114; pilin; 1.
 DR PROSITE; PS00409; PROKAR_NTER_METHYL, PARTIAL.
 KW Fimbria; 3D-structure.
 FT NON_TER 1 1
 FT DISULFID 8 21
 SQ SEQUENCE 23 AA; 2415 MW; DOBE7751AF041CF CRC64;

Query Match 20.6%; Score 135; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 1.2e-06;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 DVNGMSCATYVDKFRPNCCTD 127
 DB 1 DVNGMSCATYVDKFRPNCCTD 23

RESULT 11
 FMI_MORBO STANDARD; PRT; 159 AA.
 AC P20657;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE FIBRIAL PROTEIN I PRECURSOR (ALPHA PILIN) (I PILIN).
 OS Moraxella bovis.
 OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae; Moraxella.
 OX NCBI_TaxID=476;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EP63;
 RX MEDLINE=90094235; PubMed=2403542;
 RA Fulk K.A., Marrs C.F., Stevens S.P., Green M.R.;
 RT "Sequence analysis of the inversion region containing the pilin genes
 RT of Moraxella bovis.";
 RL J. Bacteriol. 172:310-316(1990).
 RN [2]
 RP SEQUENCE OF 7-159.
 RX MEDLINE=89010522; PubMed=2902184;
 RA Ruehl W.W., Marrs C.F., Fernandez R., Falkow S., Schoonnik G.K.;
 RT "Purification, characterization, and pathogenicity of Moraxella bovis
 RT pilin.";
 RL J. Exp. Med. 168:983-1002(1988).
 CC -1- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
 CC NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH. THEY
 CC CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
 CC CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.
 CC -1- MISCELLANEOUS: MORAXELLA BOVIS CAN EXPRESS EITHER A Q OR A I
 CC PILIN, THE INVERSION OF 2 KB OF DNA DETERMINES WHICH PILIN IS
 CC EXPRESSED.
 CC -1- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.

 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DR EMBL; M32345; -; NOT_ANNOTATED_CDS.
 DR PIR; J10071; J10071.
 DR HSSP; F02974; IAY2.
 DR InterPro; IPR001082; Pilin.
 DR InterPro; IPR001120; Prok_N_methyltn.
 DR Pfam; PF00114; pilin; 1.
 DR PRODOM; PD000666; pilin; 1.
 DR PROSITE; PS00409; PROKAR_NTER_METHYL, 1.
 KW Fimbria; Methylation.
 FT PROPEP 1 6
 FT CHAIN 7 159
 FT MOD_RES 7 7 FIBRIAL PROTEIN I.
 FT MOD_RES 7 7 METHYLATION.
 FT CONFLICT 159 159 K -> KSK (IN REF. 2).

RESULT	14
EMCD_PSEAE	
ID	EMCD_PSEAE
AC	STANDARD;
DT	P17837;
DT	01-AUG-1990 (Rel. 15, Created)
DT	01-AUG-1990 (Rel. 15, Last sequence update)
DE	01-FEB-1994 (Rel. 28, Last annotation update)
GN	FIMBRIAL PROTEIN PRECURSOR (PILIN) (STRAIN CD).
OS	PILA OR FIMA.
OC	Pseudomonas aeruginosa.
OC	Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC	Pseudomonas.
OX	NCBI_TaxID=287;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	STRAIN=CD;
RX	MEDLINE=88138467; PubMed=2893774;
RA	Pasloske B.L., Joffe A.M., Sun Q., Volpel K., Paranchych W.,
RA	Etekarha F., Speert D.P.;
RT	"Serial isolates of Pseudomonas aeruginosa from a cystic fibrosis
RT	patient have identical pilin sequences.";
RL	Infect. Immun. 56:665-672(1988).
CC	-1- SUBUNIT. THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
CC	NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
CC	CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
CC	-1- SIMILARITY. BELONGS TO THE N-ME-PHE PILI FAMILY. ALMOST IDENTICAL
CC	TO PA103 PILIN.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation
CC	the European Bioinformatics Institute. There are no restrictions on
CC	use by non-profit institutions as long as its content is in no way
CC	modified and this statement is not removed. Usage by and for commercial
CC	entities requires a license agreement (See http://www.isb-slb.ch/announce/
CC	or send an email to license@isb-slb.ch).
CC	-----
DR	EMBL; M24281; AAA25945.1; ALT_INIT.
DR	PIR; A43504; A43504.
DR	HSSP; P02973; INTL.
DR	InterPro; IPR001082; Pilin.
DR	InterPro; IPR001120; Prok_N_methyltn.
DR	Pfam; PF00114; pilin.1.
DR	ProDom; PD000666; Pilin.1.
DR	PROSITE; PS00409; PROKAR_NTER_METHYL.1.
KW	Fimbria; Methylation.
FT	PROPEP
FT	1
FT	6
FT	150
FT	7
FT	7
FT	134
FT	147
FT	15743
FT	MM; E14316996F270F5C CRC64;
FT	SEQUENCE
FT	150
FT	7
FT	7
FT	134
FT	147
FT	15743
FT	MM; E14316996F270F5C CRC64;
FT	SEQUENCE
FT	150
FT	7
FT	7
FT	134
FT	147
FT	15743
FT	MM; E14316996F270F5C CRC64;
FT	SEQUENCE
FT	150
FT	7
FT	7
FT	134
FT	147
FT	15743
FT	MM; E14316996F270F5C CRC64;
FT	SEQUENCE
FT	150
FT	7
FT	7
FT	134
FT	147
FT	15743
FT	MM; E14316996F270F5C CRC64;
FT	SEQUENCE
FT	150
FT	7
FT	7
FT	134
FT	147
FT	15743
FT	MM; E14316996F270F5C CRC64;
FT	SEQUENCE
FT	150
FT	7
FT	7
FT	134
FT	147
FT	15743
FT	MM; E14316996F270F5C CRC64;
FT	SEQUENCE
FT	150
FT	7
FT	7
FT	134
FT	147
FT	15743
FT	MM; E14316996F270F5C CRC64;
FT	SEQUENCE
FT	150
FT	7
FT	7
FT	134
FT	147
FT	15743
FT	MM; E14316996F270F5C CRC64;
FT	SEQUENCE
FT	150
FT	7
FT	7
FT	134
FT	147
FT	15743
FT	MM; E14316996F270F5C CRC64;
FT	SEQUENCE
FT	150
FT	7
FT	7
FT	134
FT	147
FT	15743
FT	MM; E14316996F270F5C CRC64;
FT	SEQUENCE
FT	150
FT	7
FT	7
FT	134
FT	147
FT	15743
FT	MM; E14316996F270F5C CRC64;
FT	SEQUENCE
FT	150
FT	7
FT	7
FT	134
FT	147

Query Match	Similarity	Score	DB 1	Length	150
Best Local	Similarity	27.1%	Pred. No. 0.00057		
Matches	35	Conservative	18	Mismatches	49
				Indels	27
				Gaps	4
QY	8	SKSOVSRYVAEAGSKTAVEACLODGRNAVGTAAAGCCDGAATGSSLTNG-ASQTSQTLPT	66		
	: :	: :			
Db	35	ARSEASASALATINPLKKTIVREEL-----SRGIAGSKILLICTASTDNT--T	78		
QY	67	NTGVQVLDPLLTQTTIATFENG-----ASAATSGTILTWTRVNGSGWCATTV	116		
	: :	: :			
Db	79	YVGIDERANKLGTAVAVTILKNDGDCIVKTFEATGSSPNACKKEITLNRFAEVEWTCSTSQ	138		
QY	117	DAKFPNPGC	125		
	: :	: :			
Db	139	EEMFIPKGC	147		

RESULT	1	
EMPA_PSEAE		
ID	EMPA_PSEAE	STANDARD;
AC	P02973; Q53390;	PRT; 150 AA.
DT	21-JUL-1986 (Rel. 01, Created)	
DT	01-NOV-1990 (Rel. 16, last annotation update)	
DT	01-NOV-1997 (Rel. 35, last annotation update)	
DE	FLIBRIAL PROTEIN PRECURSOR (PILIN) (STRAIN PAK).	
GN	PILA OR FIMA.	
OS	<i>Pseudomonas aeruginosa</i> .	
OC	Bacteria; Proteobacteria; gamma subdivision; <i>Pseudomonadaceae</i> ;	
OC	<i>Pseudomonas</i> .	
OX	NCBI_TaxID=287;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RP	STRAIN=PAK;	
RX	MEDLINE=85180008; PubMed=2985436;	
RA	Pasloske B.L., Finlay B.B., Paranchych W.;	
RT	"Cloning and sequencing of the <i>Pseudomonas aeruginosa</i> PAK pilin gene.";	
RL	J. Biol. Chem. 261:15703-15708(1986).	
RN	[3]	
RP	SEQUENCE OF 7-150.	
RC	STRAIN=PAK;	
RX	MEDLINE=83158129; PubMed=6131838;	
RA	Sastry P.A., Pearlstone J.R., Smillie L.B., Paranchych W.;	
RT	"Amino acid sequence of pilin isolated from <i>Pseudomonas aeruginosa</i> PAK.";	
RL	FEBS Lett. 151:253-256(1983).	
RN	[4]	
RP	SEQUENCE OF 128-150 FROM N.A.	
RX	MEDLINE=94103636; PubMed=7903973;	
RA	IPATSG;	
RT	"A multicenter comparison of methods for typing strains of <i>Pseudomonas aeruginosa</i> predominantly from patients with cystic fibrosis. The International <i>Pseudomonas aeruginosa</i> Typing Study Group.";	
RL	J. Infect. Dis. 169:134-142(1994).	
RN	[5]	
RP	STRUCTURE BY NMR OF 134-150.	
RX	MEDLINE=94079874; PubMed=8257679;	
RA	McInnes C., Soennichsen F.D., Kay C.M., Hodges R.S., Sykes B.D.;	
RT	"NMR solution structure and flexibility of a peptide antigen representing the receptor binding domain of <i>Pseudomonas aeruginosa</i> .";	
RL	Biochemistry 32:13493-13440(1993).	
CC	-1 SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4 NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.	
CC	-1 SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.	
CC	-----	
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	
CC	-----	
DR	EMBL; M14849; AAA25955.1; -	
DR	EMBL; X02402; CAA26248.1; -	
DR	EMBL; S67807; CAB32859.1; -	
DR	PIR; A03497; YOPSPA.	
DR	PIR; A24603; A24603.	
DR	PIR; A28780; A28780.	

DR PDB: 1PAJ; 31-JAN-94.
 DR PDB: 1PAK; 31-JAN-94.
 DR PDB: INIL; 29-JAN-96.
 DR PDB: INIM; 29-JAN-96.
 DR InterPro: IPR001082; PiliN.
 DR InterPro: IPR001120; Prok_N_methyltn.
 DR Pfam: PF00114; PiliN; 1.
 DR PRODOM: PD000666; PiliN; 1.
 DR PROSITE: PS00409; PROKAR_NTER_METHYL; 1.
 DR Fimbrin; Methylation; 3D-structure.
 KW PROPEP 1 6
 FT CHAIN 7 150 FIMBRIN PROPEIN.
 FT MOD_RES 7 7 METHYLATION (BY SIMILARITY).
 FT DISULFID 135 148
 FT CONFLICT 90 90 T -> TS (IN REF. 3).
 FT CONFLICT 101 103 TAD -> DTA (IN REF. 3).
 FT CONFLICT 128 128 A -> D (IN REF. 4).
 FT CONFLICT 150 150 R -> K (IN REF. 2).
 SO SEQUENCE 150 AA; 15650 MW; COE35B69FD6FBE84 CRC64;

Query Match 17.1%; Score 112; DB 1; Length 150;
 Best Local Similarity 30.1%; Pred. No. 0.0012;
 Matches 37; Conservative 16; Mismatches 58; Indels 12; Gaps 5;

OY 8 SRSQVSRVMAEAGSLKTRAVEACLODG---RTAVGTAGQCDPGATGSSLLTGASQTSQTL 64.
 DB 35 ARSEGASALASVNPDKTTVEEALSRGWSVKSQGTG-----EDATKKEVPLGVAAADANKL 88
 OY 65 PTNTGVPOVLDPLTFTQFTIITFGNGASAAISGOTLTWTRD-VNGGWSGATTVDKFRPN 123
 DB 89 GTIAKPPADG-TADITLFTMG-GAGPRNKGKIIITLRTAADGLWKCISDQDEQFLPK 146
 OY 124 GCT 126
 DB 147 GCS 149

Search completed: February 8, 2002, 15:34:23
 Job time: 548 sec

Result No.	Score	Query Match	Length	DB	ID	Description
1	270	41.3	131	2	09AP36	09AP36 bacteroides
2	270	41.3	157	2	059336	059336 dictiobact
3	243	37.2	134	2	09SA4E1	09SA4E1 bacteroides
4	235.5	36.0	130	2	09SA4E2	09SA4E2 bacteroides
5	152	23.2	157	2	059503	059503 moraxella b
6	150.5	23.0	154	2	059794	059794 pseudomonas
7	144	22.0	143	2	048936	048936 moraxella b
8	142.5	21.8	156	2	059507	059507 moraxella b
9	138	21.1	159	2	059505	059505 moraxella b
10	129	19.7	159	2	060163	060163 moraxella b
11	128.5	19.6	135	2	056800	056800 xanthomonas
12	128.5	19.6	160	2	059504	059504 moraxella b
13	127	19.4	158	2	059508	059508 moraxella b
14	124.5	19.0	158	2	059501	059501 moraxella b
15	123.5	18.9	145	2	09APK5	09APK5 xanthomonas
16	123	18.8	140	2	09AF61	09AF61 pseudomonas
17	122.5	18.7	146	2	052613	052613 xanthomonas
18	121.5	18.6	150	2	059795	059795 pseudomonas
19	119.5	18.3	139	2	09ZEL3	09ZEL3 pseudomonas

20	110.5	16.9	130	2	09APJ4	09APJ4 xanthomonas
21	109	16.7	147	2	030583	030583 acinetobact
22	107.5	16.4	153	2	09XAG7	09XAG7 vibrio chol
23	107.5	16.4	167	2	09KPE5	09KPE5 vibrio chol
24	107	16.4	148	2	09PAH6	09PAH6 xylella fast
25	101.5	15.5	136	2	056799	056799 xanthomonas
26	96.5	14.8	116	2	09APJ3	09APJ3 xanthomonas
27	96.5	14.8	187	2	09PTW8	09PTW8 xylella fast
28	95	14.5	188	2	09WYV3	09WYV3 bacteroides
29	94	14.4	148	2	09PAH9	09PAH9 xylella fast
30	91.5	14.0	158	2	054650	054650 bacteroides
31	91	13.9	151	2	09ZAR0	09ZAR0 aeromonas s
32	90.5	13.8	357	3	074236	074236 fusarium ox
33	89	13.6	175	2	09S4E5	09S4E5 bacteroides
34	88	13.5	711	5	022783	022783 caenorhabdi
35	87.5	13.4	133	2	09S4E9	09S4E9 bacteroides
36	87	13.3	144	2	09L588	09L588 bacteroides
37	87	13.3	144	2	P78000	P78000 kingella de
38	87	13.3	471	3	09HEH8	09HEH8 trichoderma
39	86.5	13.2	483	3	09MWS1	09MWS1 pseudomonas
40	86	13.1	455	2	051835	051835 aeromonas s
41	86	13.1	445	2	09LBN6	09LBN6 leptothrix
42	84.5	12.9	133	2	09S4E8	09S4E8 bacteroides
43	84.5	12.9	264	5	000789	000789 plasmodium
44	84	12.8	252	2	09EWY0	09EWY0 streptomyces
45	83	12.7	262	5	09TWY6	09TWY6 plasmodium

ALIGNMENTS

	RESULT	1	
Q9AP36			
ID	Q9AP36	PRELIMINARY;	PRT; 131 AA.
AC	Q9AP36;		
DT	01-JUN-2001 (TREMBLrel. 17, Created)		
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)		
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)		
DE	FIMBRIAL SUBUNIT (FRAGMENT).		
GN	FIMA.		
OS	Bacteroides nodosus (Dichelobacter nodosus).		
OC	Bacteria; Proteobacteria; gamma subdivision; Cardiobacteriaceae		
CC	Dichelobacter.		
OX	NCBI_TaxID=870;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Zhou H., Hickford J.G.H.;		
RT	"Dichelobacter nodosus fimbrial subunit gene.";		
RL	Submitted (OCT-2000) to the EMBL/GenBank/DDU databases.		
DR	EMBL: AF316610; AKK00323.1; ..		
FT	NON_TER		
EQ	SEQUENCE 131 AA; 1993 MW; 5406DD20DCCECB1ABD CRC64;		

Query Match	Score	DB 2;	Length
41.38;	270;	DB 2;	Length 131;

Matches 58; Conservative 21; Mismatches 33; Indels 16; Gaps 4;

```

0y      8 SRSQVSRHMAAGSILKTAVEACLODDGRAVTAAGCDDPGATGSSLL----TGASQNSQI 63
      9 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      10 ARSQVSRHMSSTGGMRTALIEVCVLDK-----EADKCEIGWTSNLLDGEPTAETSTAA 64

0y      64 LPTNPGV---PQVLDPLTTOITLITAFNGASAAISQITLTTRDYNGGSCATYYDAK 119
      65 ATGGTGITIKYVPVAD---DEGNITVATFNGRNAALIKPQITLTMSRSKEGTTCAATYVAK 123

```

QY	120	FRPNCCTD	127
		1:1111	
Dd	122	FQPTGCKD	129

RESULT 2
Q59336

ID	059336	PRELIMINARY:	PRT:	157 AA.
AC	059336:			
DT	01-NOV-1996	(TREMBLrel. 01, Created)		
DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)		
DT	01-JUN-2001	(TREMBLrel. 17, Last annotation update)		
DE	PILIN.			
D5	Dichelobacter nodosus H1.			
OC	Bacteria; Proteobacteria; gamma subdivision; Cardiobacteriaceae;			
OC	Dichelobacter.			
OX	NCBI_TaxID=46911;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	STRAIN=BN265;			
RA	MEDLINE=90155189; PubMed=2621448;			
RT	Hoyme P.A., Elleman T.C., McKern N.M., Stewart D.J.:			
RT	"Sequence of pilin from <i>Bacteroides nodosus</i> 351 (Serogroup H) and			
RT	implications for serogroup classification.";			
RL	J. Gen. Microbiol. 135:1113-1122(1989).			
CC	-1 SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4			
CC	NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY			
CC	CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL			
CC	CONFORMATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS (BY			
CC	SIMILARITY).			
CC	-1 SIMILARITY: BELONGS TO THE FIMBRIAL PROTEIN (N-ME-PHE)PILIN			
CC	FAMILY.			
DR	EMBL: M26979; AAA98742.1. -			
DR	HSSP: 053391; 1KB8.			
DR	InterPro: IPR001082; PILIN.			
DR	InterPro: IPR001120; PROK_N_methyln.			
DR	Pfam: PF00014; pilin; 1.			
DR	ProDom: PD00066; pilin; 1.			
DR	PROSITE: PS00409; PROKAR_NTER_METHYL. 1.			
KW	Fimbria; Methylation			
FT	MOD RES 8			
FT	METHYLATION (BY SIMILARITY).			
SO	SEQUENCE 157 AA; 16702 MW; 63601952511E0967 CRC64;			

```

Query Match Similarity 41.3%; Score 270; DB 2; Length 157;
Best Local Similarity 45.3%; Pred. No. 2, 1e-15;
Matches 58; Conservative 21; Mismatches 33; Indels 16; Gaps
4

QY 8 SRSQSVRNAVAAAGSLKTAVEACLDQDERTAVGTAAAGCCDPAATGSSIL-----TCASQTSQT 63
Db 36 ARSQSVRNAVSENGQMTALTEICVLDR-----EADKCFIGTWSNLLDDEFTAGTSTAA 90
QY 64 LPTNTEGV-----POYDPLTQTITIAFTENGSAASALISQTLTWTRDYNWGWSQCATVDAK 119
Db 91 ARGQGTITITIKYPVAAD---DEGNIVATFGFRNMAAAIKPQLTWSRSKESSTWCATTVAK 147
QY 120 FRPNCGT 127
Db 148 FQPTGCKD 155

RESULT 3
09S4EI ID 09S4EI PRELIMINARY; PRT; 134 AA.
AC 09S4EI
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE FIMBRIAL SUBUNIT (FRAGMENT).
GN FIMA.
OS Bacteroides nodosus (Dichelobacter nodosus).
OC Bacteria; Proteobacteria; gamma subdivision; Cardiobacteriaceae;
CC Dichelobacter.
OX NCBI_TaxID=870;
RX [1]
RA SEQUENCE FROM N.A.
RP Zhou H., Hickford J.G.H.;
RT "Dichelobacter nodosus fimbrial subunit gene (fima).";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
EMBL AF146891; AAD43088.1; -

```

DR HSSP: Q53391; 1KR8.
DR InterPro: IPR001082; Pili_n.
DR Pfam: PF00114; pili_n; 1.
DR ProDom: PD000666; Pili_n; 1.
FT NON_TER 1 1
SQ SEQUENCE 134 AA; 14409 MW; EFB9AB2C330CF7E CRC64

Query Match	37.2%	Score 243;	DB 2;	Length 134;
Best Local Similarity	42.5%;	Pred. No. 3.2e-13;		
Matches 54;	Conservative 17;	Mismatches 44;	Indels 12;	Gaps 3

```

QY      8  SRQSVRYMAMGSLKTKAVCELODGRVANGOCDEPGATGSSLLTGASQTSQTLPTN  67
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db     10  ARQSVRYMSTGOMRALIETCLDGR-----KADECFIQWTSNLLGAGSPSSNDST  64
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
QY      68  TGVF-----PLTQTTTATFGNGASAAISQOTLTWRDVGNGSCATTYDAKE  120
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db      65  ADDGGGGLVIDYKLEADATNTTATFGONAAATLHGKALKKTRDPRATVSCSDVELKE  124
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
QY     121  RPNCGTID  127
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db     125  RPTGCKD  131
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

```

```

RESULT 4
Q9SAE2
ID Q9SAE2 PRELIMINARY; PRT; 130 AA.
Q9SAE2;
DT 01-MAY-2000 (TREMBLrel. 13. Created)
DT 01-MAY-2000 (TREMBLrel. 13. Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE FIMBRIAL SUBUNIT (FRAGMENT).
GN FIMA.
OS Bacteroides nodosus (Dichelobacter nodosus).
OC Bacteria; Proteobacteria; gamma subdivision; Cardiobacteriaceae;
OC Dichelobacter.
OX NCBI_TaxID=870;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhou H., Hickford J.G.H.;
RT "Dichelobacter nodosus fimbrial subunit gene (fima).";
RL Submitted (APR-1999) to the EMBL/Genbank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RA Zhou H., Hickford J.G.H.;
RT "Dichelobacter nodosus fimbrial subunit gene.";
RL Submitted (OCT-2000) to the EMBL/Genbank/DBJ databases.
EMBL: AF146890; AAD3087.1; -
EMBL: AF316611; AKK0524.1; -
DR InterPro: IPR001082; Piliin.
DR Pfam: PF00114; Piliin; 1.
DR ProDom: PD000666; Piliin; 1.
FT NON_TER 1
SQ SEQUENCE 130 AA; 13838 MW; 0978D2488FEA6C9D CRC64;

```

	Query Match	36.0%;	Score 235.5;	DB 2;	Length 130;	
	Best Local Similarity	42.4%;	Pred. No. 1.3e-12;			
	Matches	53;	Conservative	17;	Mismatches 42;	Indels 13; Gaps 4;
OY	8 SRSQVSRYVAEEGSLKTAVEACTCLOGRTAVGTAAOCCDPGATGSSLL--TGASQTSTQLP	65				
	: :: ::: : :::					
Dd	10 ASQVSRWASEFGOMRTALETCLDGGK-----EGKDCEFGWTTSNLIILAAAGSTTNMATA	64				
OY	66 TMTG-----VPVDLPLTTTOTIITATFGGSAASISQTLFTWRPVNGWSGCATTVDAKE	120				
	: : : : : : : : : : : : : : : : :					
Dd	65 ADPGGGGLINIAVALES-TAENKIETAFQNNAAATIGHKKLTWTRSPDEATWSCSTDVERF	123				
OY	121 RPNGC 125					
	: : : : : : : : : : : : : : :					
Dd	124 KPTGC 128					

```

RESULT 5
ID 059503 PRELIMINARY; PRT; 157 AA.
AC 059503;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE PREPILIN.
OS Moraxella bovis.
OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae; Moraxella.
OX NCBI_Taxid=476;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FL462 / SEROGROUP G;
RX MEDLINE=94327452; PubMed=8051000;
RA Atwell J.L., Tennent J.M., Lepper A.W., Elleman T.C.;
RT "Characterization of pilin genes from seven serologically defined
RT prototype strains of Moraxella bovis.";
RL J. Bacteriol. 176:4875-4882(1994).
CC -1- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
CC NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
CC CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
CC CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS (BY
CC SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE FIMBRIAL PROTEIN (N-ME-PHE)PILIN
CC FAMILY.
CC EMBL; L32966; AAA53559.1;
CC InterPro; IPR001082; Pilin.
CC Pfam; PF00114; Pilin; 1.
CC ProDom; PD000666; Pilin; 1.
CC PROSITE; PS00409; PROKAR_NTER_METHYL. 1.
CC Fimbrin; Methylation.
CC MOD_RES 7 METHYLATION (BY SIMILARITY).
CC FT MOD_RES 7
CC SEQUENCE 157 AA; 16327 MW; EEAFCADF382430D2 CRC64;

Query Match 23.2%; Score 152; DB 2; Length 157;
Best Local Similarity 31.0%; Pred. No. 1.4e-05;
Matches 44; Conservative 18; Mismatches 38; Indels 42; Gaps 4;

OY 8 SRSQVRYVAEAGSLKTVACLDGRTAVGTAACQCPGATGSSLLTGASQTSQTLPTN 67
ID 059794 PRELIMINARY; PRT; 154 AA.
AC 059794;
DT 01-JUN-1998 (TREMblrel. 06, Created)
DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE FIMBRIAL PROTEIN PRECURSOR (PILIN) (STRAIN 577B).
GN PILA OR FIMA.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_Taxid=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=577B;
RX MEDLINE=94131566; PubMed=7507890;
RA Castrie P.A., Deal C.D.;

```

```

RT "Differentiation of Pseudomonas aeruginosa pili based on sequence and
RT B-cell epitope analyses.";
RL Infect. Immun. 62:371-376(1994).
CC -1- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
CC NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
CC CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
CC CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.
CC -1- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
CC EMBL; S68101; AAC60461.1;
CC HSSP; P02974; 2PII.
CC InterPro; IPR001082; Pilin.
CC Pfam; PF00114; Pilin; 1.
CC ProDom; PD000666; Pilin; 1.
CC PROSITE; PS00409; PROKAR_NTER_METHYL. 1.
CC Fimbrin; Methylation.
CC MOD_RES 7 154 FIMBRIAL PROTEIN.
CC FT CHAIN 7 154 BY SIMILARITY.
CC FT DISULF 133 151 METHYLATION (BY SIMILARITY).
CC FT MOD_RES 7 7
CC SEQUENCE 154 AA; 16317 MW; 52A0A56725135719 CRC64;

Query Match 23.0%; Score 150.5; DB 2; Length 154;
Best Local Similarity 32.8%; Pred. No. 1.8e-05;
Matches 40; Conservative 20; Mismatches 45; Indels 17; Gaps 4;

OY 8 SRSQVRYVAEAGSLKTVACLDGRTAVGTAACQCPGATGSSLLTGASQTSQ 62
ID 048936 PRELIMINARY; PRT; 143 AA.
AC 048936;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE PILIN (FRAGMENT).
OS Moraxella bovis.
OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae; Moraxella.
OX NCBI_Taxid=476;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D2D SEROGROUP C;
RX MEDLINE=94327452; PubMed=8051000;
RA Atwell J.L., Tennent J.M., Lepper A.W., Elleman T.C.;
RT "Characterization of pilin genes from seven serologically defined
RT prototype strains of Moraxella bovis.";
RL J. Bacteriol. 176:4875-4882(1994).
CC EMBL; L32967; AAA53564.1;
CC InterPro; IPR001082; Pilin.
CC Pfam; PF00114; Pilin; 1.
CC ProDom; PD000666; Pilin; 1.
CC MOD_RES 143 143
CC FT NON_TER 143
CC SEQUENCE 143 AA; 15158 MW; F32FD85A6DB8D60C CRC64;

Query Match 22.0%; Score 144; DB 2; Length 143;
Best Local Similarity 31.5%; Pred. No. 5.7e-05;
Matches 40; Conservative 18; Mismatches 57; Indels 12; Gaps 3;

OY 8 SRSQVRYVAEAGSLKTVACLDGRTAVGTAACQCPGATGSSLLTGASQTSQTLPTN 67
ID 048936 PRELIMINARY; PRT; 143 AA.
AC 048936;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE PILIN (FRAGMENT).
OS Moraxella bovis.
OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae; Moraxella.
OX NCBI_Taxid=476;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D2D SEROGROUP C;
RX MEDLINE=94327452; PubMed=8051000;
RA Atwell J.L., Tennent J.M., Lepper A.W., Elleman T.C.;
RT "Characterization of pilin genes from seven serologically defined
RT prototype strains of Moraxella bovis.";
RL J. Bacteriol. 176:4875-4882(1994).
CC EMBL; L32967; AAA53564.1;
CC InterPro; IPR001082; Pilin.
CC Pfam; PF00114; Pilin; 1.
CC ProDom; PD000666; Pilin; 1.
CC MOD_RES 143 143
CC FT NON_TER 143
CC SEQUENCE 143 AA; 15158 MW; F32FD85A6DB8D60C CRC64;

```

```

Db 17 SKSQTRVVGELAGTAIDALFDKTPVLNKAASDPTENENIGLTTSDTKPRSNLLAE 76
Ox 68 TGVPQVLDPLTQTITIAFPGNGASAISSQTLTTRDVNGSGSCATTVDA-----K 119
Db 77 NGISLIED--GTDLVAKGILGRNANDICTEYVNOIRDKNGNSC--TYKGVNKGWKDK 132
Ox 120 FRPNGCT 126
Db 133 FIPSGCT 139

RESULT 8
Ox 039507 PRELIMINARY; PRT; 156 AA.
AC 039507;
DT 01-NOV-1996 (TREMBLREL. 01, Created)
DT 01-NOV-1996 (TREMBLREL. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLREL. 17, Last annotation update)
DE PILIN.
OS Moraxella bovis.
OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae; Moraxella.
OX NCBI_TaxID=476;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90256243; PubMed=1971258;
RA Elleman T.C., Hoyne P.A., Lepper A.W.;
RT "Characterization of the pilin gene of Moraxella bovis Dalton 2d and
RT expression of pilI from M. bovis in Pseudomonas aeruginosa."
RL Infect. Immun. 58:1678-1684(1990).
CC -1- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
CC NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
CC CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
CC CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS (BY
CC SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE FIMBRIAL PROTEIN (N-ME-PHE)PILIN
CC FAMILY.
DR EMBL: M92155; AAA53087.1; -.
DR InterPro: IPR001082; Pilin.
DR Pfam: PF00114; pilin; 1.
DR ProDom: PD000666; pilin; 1.
DR PROSITE: PS00409; PROKAR_NTER_METHYL. 1.
DR Fimbrin; Methylation.
KW MOD_RES
FT SEQUENCE 156 AA; 15941 MW; EB281DA663B9B3C9 CRC64;

Query Match 21.8%; Score 142.5; DB 2; Length 156;
Best Local Similarity 30.2%; Pred. No. 8.3e-05;
Matches 42; Conservative 15; Mismatches 43; Indels 39; Gaps 4;

Ox 8 SRSQSVRAAEAGSLKTAVEACLDGRTAVGTAAGCCDPCGATG-----SS 52
Db 35 SKSQTRVVGELAAKKTADALFEKTPV-----VNSAGIAEVDLGLGEAATPPSN 88
Ox 53 LITGASQTSQTLPTNTGVPOVLDPLTQTITIAFPGNGASAISSQTLTTRDVNGSGSC 112
Db 89 LLSAVSFTFGKSN-----GTISGITGNANDIHCTVISOEDATGAWSC 135
Ox 113 ATTVDA-----KFRPNGCT 126
Db 136 KVTGNGTGWKDKFIPSGCT 154

RESULT 9
Ox 039505 PRELIMINARY; PRT; 159 AA.
AC 039505;
DT 01-NOV-1996 (TREMBLREL. 01, Created)
DT 01-NOV-1996 (TREMBLREL. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLREL. 17, Last annotation update)
DE PREPILIN.
OS Moraxella bovis.

```

```

OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae; Moraxella.
OX NCBI_TaxID=476;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=7AT849 / SEROGROUP E;
RX MEDLINE=94327452; PubMed=8051000;
RA Atwell J.L., Tennent J.M., Lepper A.W., Elleman T.C.;
RT "Characterization of pilin genes from seven serologically defined
RT prototype strains of Moraxella bovis."
RL J. Bacteriol. 176:4875-4882(1994).
CC -1- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
CC NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
CC CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
CC CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS (BY
CC SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE FIMBRIAL PROTEIN (N-ME-PHE)PILIN
CC FAMILY.
DR EMBL: L32972; AAA53561.1; -.
DR InterPro: IPR001082; Pilin.
DR Pfam: PF00114; pilin; 1.
DR ProDom: PD000666; pilin; 1.
DR PROSITE: PS00409; PROKAR_NTER_METHYL. 1.
DR Fimbrin; Methylation.
KW MOD_RES
FT SEQUENCE 159 AA; 16534 MW; F40828A90E93089 CRC64;

Query Match 21.1%; Score 138; DB 2; Length 159;
Best Local Similarity 30.2%; Pred. No. 0.0002;
Matches 42; Conservative 22; Mismatches 39; Indels 36; Gaps 5;

Ox 8 SRSQSVRAAEAGSLKTAVEACLDGRTAVGTAAGCCDPCGATGSSLLTGASQTSQ----- 62
Db 35 SKSQTRVVGELAAKKTADALFEKTPV-----LNFASTSKENIGL 78
Ox 63 TLPNTGVPO--VLDPLT-----QTTIAFPGNGASAISSQTLTTRDVNGSGSC- 112
Db 79 TTSEMSATPRSLMSESVSLEGGDSNGGSSISATLGNANKDIKTVISONRTTDSWICE 138
Ox 113 ----ATTVDKFRPNGCT 126
Db 139 VDGKAPRYKAKFTPAGCT 157

RESULT 10
Ox 060163 PRELIMINARY; PRT; 159 AA.
AC 060163;
DT 01-NOV-1996 (TREMBLREL. 01, Created)
DT 01-NOV-1996 (TREMBLREL. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLREL. 17, Last annotation update)
DE PREPILIN.
OS Moraxella bovis.
OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae; Moraxella.
OX NCBI_TaxID=476;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=RS93L / SEROTYPE D;
RX MEDLINE=94327452; PubMed=8051000;
RA Atwell J.L., Tennent J.M., Lepper A.W., Elleman T.C.;
RT "Characterization of pilin genes from seven serologically defined
RT prototype strains of Moraxella bovis."
RL J. Bacteriol. 176:4875-4882(1994).
CC -1- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
CC NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
CC CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
CC CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS (BY
CC SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE FIMBRIAL PROTEIN (N-ME-PHE)PILIN
CC FAMILY.
DR EMBL: L32971; AAA53563.1; -.
DR Fimbrin; Methylation.
KW MOD_RES
FT SEQUENCE 159 AA; 16534 MW; F40828A90E93089 CRC64;

```

DR InterPro: IPR001082; Piliin.
 DR InterPro: IPR001120; Prok_N_methyltn.
 DR Pfam: PF00114; Piliin; 1.
 DR ProDom: PD000666; Piliin; 1.
 DR PROSITE: PS00409; PROKAR_NTER_METHYL; 1.
 KW Fimbria; Methylation.
 FT MOD_RES 7 METHYLATION (BY SIMILARITY).
 SQ SEQUENCE 159 AA: 16459 MW; F2113DD7ECD578FC CRC64;

Query Match 19.7%; Score 129; DB 2; Length 159;
 Best Local Similarity 30.7%; Pred. No. 0.0011;
 Matches 39; Conservative 19; Mismatches 37; Indels 12; Gaps 4;

OY 8 SRSQVSRVMAEAGSLKTAVEACLDGRTAVGTAAGCCDPGATGSSLLTGASQTSQTLPTN 67
 DB 35 SKSQTRVVGELAGKTAVDALFEKPEV-LQANNADTSKEDIGLPTDSNNPRSNLMSN 93
 OY 68 TGVPLVDPLTTQTITITFGNGASAAISGQTLTTRDVNGWGCATTYDA-----K 119
 DB 94 VELG-ESATSSAGITITGLTRANKDITGAKIMQNRADGVWC--TIDGSAATGMKDK 150
 OY 120 FRPNGCT 126
 DB 151 FIPFGCT 157

RESULT 11
 O56800 PRELIMINARY; PRT: 135 AA.

ID O56800
 AC O56800:
 DT 01-NOV-1996 (TREMBLrel.. 01, Created)
 DT 01-NOV-1996 (TREMBLrel.. 01, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel.. 17, Last annotation update)
 DE FIMBRILIN.
 GN FIMB.
 OS Xanthomonas campestris.
 OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
 OC Xanthomonas.
 OX NCBI_TaxID=339;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=3240 (NCPPB);
 RX MEDLINE=97175558; PubMed=9023213;
 RA Ojnen-Reus T., Kalkkunen N., Westerlund-wikstrom B., van Doorn J.,
 Hahtela K., Nurmiaho-Lassila E.L., Wengelnik K., Bonas U.,
 Korhonen T.K.;
 RA "Characterization of the fima gene encoding bundle-forming fimbriae of
 RT the plant pathogen Xanthomonas campestris pv. vesicatoria";
 RL J. Bacteriol. 179:1280-1290(1997).
 DR EMBL; Z48759; CA88681.1;
 DR InterPro: IPR001082; Piliin.
 DR Pfam: PF00114; Piliin; 1.
 DR ProDom: PD000666; Piliin; 1.
 SQ SEQUENCE 135 AA: 13854 MW; 5A5045709831860B CRC64;

Query Match 19.6%; Score 128.5; DB 2; Length 135;
 Best Local Similarity 31.9%; Pred. No. 0.001;
 Matches 38; Conservative 18; Mismatches 44; Indels 19; Gaps 5;

OY 8 SRSQVSRVMAEAGSLKTAVEACLDGRTAVGTAAGCCDPGATGSSLLTGASQTSQTLPTN 67
 DB 35 AAQQLTAALAEALPKGTITTEAAVQD---GTNPVTDAPYIGLLSTFCAVSAVL-SS 88
 OY 68 TGVPLVDPLTTQTITITFGNGASAAISGQTLTTRDVNGWGC-ATTVDKFRPNCG 125
 DB 89 TGVAEI--SCTIQ-----GSALVSGMDLKLRSADGWCIDGSAFDAKYPACG 135

RESULT 12
 O59504 PRELIMINARY; PRT: 160 AA.

AC O59504:
 DT 01-NOV-1996 (TREMBLrel.. 01, Created)
 DT 01-NOV-1996 (TREMBLrel.. 01, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel.. 17, Last annotation update)
 DE PREPILIN.
 OS Moraxella bovis.
 OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae; Moraxella.
 OX NCBI_TaxID=476;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S276R / SEROGROUP A;
 RX MEDLINE=94327452; PubMed=8051000;
 RA Atwell J.L., Tennent J.M., Lepper A.W., Elleman T.C.;
 RT "Characterization of pili genes from seven serologically defined
 RT prototype strains of Moraxella bovis.";
 RL J. Bacteriol. 176:4875-4882(1994).
 CC -1- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
 CC NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
 CC CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
 CC CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE FIMBRIAL PROTEIN (N-ME-PHE)PILIN
 CC FAMILY.
 CC EMBL; L32968; AAA53560.1;
 DR InterPro: IPR001082; Piliin.
 DR InterPro: IPR001120; Prok_N_methyltn.
 DR Pfam: PF00114; Piliin; 1.
 DR ProDom: PD000666; Piliin; 1.
 DR PROSITE: PS00409; PROKAR_NTER_METHYL; 1.
 KW Fimbria; Methylation.
 FT MOD_RES 7 METHYLATION (BY SIMILARITY).
 SQ SEQUENCE 160 AA: 16548 MW; B39939B7A10BF20B CRC64;

Query Match 19.6%; Score 128.5; DB 2; Length 160;
 Best Local Similarity 32.6%; Pred. No. 0.0012;
 Matches 44; Conservative 11; Mismatches 51; Indels 29; Gaps 4;

OY 8 SRSQVSRVMAEAGSLKTAVEACLDGRTAV--GTAAGQ-----CDPGATGSSLLTG 56
 DB 35 SKSQTRVVGELAGKTAVDALFEKRPVLAAPAGNTTENGITGTGATPRSNLMS 94
 OY 57 ASQTSQTLPTNGVQVLDPLTTQTITITFGNGASAAISGQTLTTRDVNGWGC----- 112
 DB 95 AVALGEGKNNAG-----TITGTLGNRANKDIAGEIISROOGVWCIDK 142
 OY 113 --ATTVDKFRPNCG 125
 DB 143 KTAPEKMKKFIPTGC 157

RESULT 13
 O59508 PRELIMINARY; PRT: 158 AA.

ID O59508
 AC O59508:
 DT 01-NOV-1996 (TREMBLrel.. 01, Created)
 DT 01-NOV-1996 (TREMBLrel.. 01, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel.. 17, Last annotation update)
 DE PREPILIN.
 OS Moraxella bovis.
 OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae; Moraxella.
 OX NCBI_TaxID=476;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=3W07 / SEROGROUP B;
 RX MEDLINE=94327452; PubMed=8051000;
 RA Atwell J.L., Tennent J.M., Lepper A.W., Elleman T.C.;
 RT "Characterization of pili genes from seven serologically defined
 RT prototype strains of Moraxella bovis.";
 RL J. Bacteriol. 176:4875-4882(1994).
 CC -1- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
 CC NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
 CC CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL

CC CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS (BY
CC SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE FIMBRIAL PROTEIN (N-ME-PHE)PILIN
CC FAMILY.
DR EMBL: L32969; AAA53565.1; -
DR InterPro: IPR001082; Pilin.
DR InterPro: IPR001120; Prok_N_methyltn.
DR Pfam: PF00114; pilin; 1.
DR ProDom: PD000666; pilin; 1.
DR PROSITE: PS00409; PROKAR_NTER_METHYL. 1.
KM Fimbria: Methylation.
FT MOD_RES 7
SQ SEQUENCE 158 AA; 16590 MW; 5958DC65678051F6 CRC64;

Query Match 19.4%; Score 127; DB 2; Length 158;
Best Local Similarity 32.3%; Pred. No. 0.0016;
Matches 43; Conservative 13; Mismatches 51; Indels 26; Gaps 4;

QY 8 SRSQVSRVMAEAGSLKTAVEACLDGRTAVGTAAGC-----DPCATGSSLLTGAS 58
DB 35 SKSQTRVVGELAGKTAVDALFECKRPVMAKTDAEEQIGLTDDGTTFRSNLMSA- 93
QY 59 QTSQLEPTNTGVPQVLDPLTQTITATFGNGASAAISQGLTWTRDVGWMSG-----A 113
DB 94 -VALNGFENNNGA-----GTIDGTIGNRANKDILCTVVTQSRSGQVWSCIYEGKG 142
QY 114 TTVDAKFRPNCGT 126
DB 143 SCWKRFKFTPGCT 155

RESULT 14
059501 PRELIMINARY; PRT; 158 AA.
AC 059501.
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE PREPILIN.
OS Moraxella bovis.
OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae; Moraxella.
OX NCBI_TaxID=476;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=218R / SEROGROUP F;
RX MEDLINE=94327452; PubMed=8051000;
RA Atwell J.U., Tennent J.M., Lepper A.W., Ellemann T.C.;
RT "Characterization of pilin genes from seven serologically defined
RT prototype strains of Moraxella bovis.";
RL J. Bacteriol. 176:4875-4882(1994).
CC -1- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
CC NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
CC CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
CC CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS (BY
CC SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE FIMBRIAL PROTEIN (N-ME-PHE)PILIN
CC FAMILY.
DR EMBL: L32965; AAA53558.1; -
DR InterPro: IPR001082; Pilin.
DR InterPro: IPR001120; Prok_N_methyltn.
DR Pfam: PF00114; pilin; 1.
DR ProDom: PD000666; pilin; 1.
DR PROSITE: PS00409; PROKAR_NTER_METHYL. 1.
KM Fimbria: Methylation.
FT MOD_RES 7
SQ SEQUENCE 158 AA; 16216 MW; 620B513CA4DC39A5 CRC64;

Query Match 19.0%; Score 124.5; DB 2; Length 158;
Best Local Similarity 31.6%; Pred. No. 0.0026;
Matches 43; Conservative 16; Mismatches 46; Indels 31; Gaps 5;

QY 8 SRSQVSRVMAEAGSLKTAVEACLDGRTAV-GTAAGCDPGATGSSLLTGASQTSQLEPT 66
DB 35 SKSQTRVVGELAGKTAVDALFECKRPVMAKTDAEEQIGLTDDGTTFRSNLMSA- 80
QY 67 NNGVQ-----VLDP---LTTQTITATFGNGASAAISQGLTWTRDVGWMSG----- 112
DB 81 AGCTPRSNLSAVTLDDGAFATGEGSIKAVLSTRANKDIAEIKRINDQGVWSCYEVA 140
QY 113 -ATTVDKFRPNCGT 126
DB 141 AGAPGKDKFTPTGCT 156
RESULT 15
09APK5
ID 09APK5 PRELIMINARY; PRT; 145 AA.
AC 09APK5.
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE FIMA PRECURSOR.
OS Xanthomonas hyacinthi.
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OX Xanthomonas.
OX NCBI_TaxID=56455;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=1157222;
RA van Doorn J.J., Hollinger T.C., Oudega B.;
RT "Analysis of the type IV fimbrial-subunit gene fima of Xanthomonas
RT hyacinthi: Application in PCR-mediated Detection of Yellow Disease in
RT Hyacinths.";
RL Appl. Environ. Microbiol. 67:598-607(2001).
DR EMBL: AF281159; AAK1163.1; -
SQ SEQUENCE 145 AA; 14911 MW; BB521BA0B59068E1 CRC64;

Query Match 18.9%; Score 123.5; DB 2; Length 145;
Best Local Similarity 29.8%; Pred. No. 0.0029;
Matches 37; Conservative 13; Mismatches 49; Indels 25; Gaps 4;
QY 8 SRSQVSRVMAEAGSLKTAVEACLDGRTAVGTAAGCDPGATGSSLLTGASQTSQLEPTN 67
DB 35 AKSQVSAGLAETTPGKVQAEFRIAGKAVTT---QADVGLQASV-----SR 78
QY 68 TGVPOVLDPLTQTITATFGNGASAAISQGLTWTR-----DVNGMSCATVDAKFR 121
DB 79 CGIAVSVPDSGAATLCTLKN--AQINGQITQWTRADRTANGTTGWCTTAVVERKL 135
QY 122 PNGC 125
DB 136 PATC 139

Search completed: February 8, 2002, 15:33:55
Job time: 560 sec

Fri Feb 8 15:44:49 2002

us-09-865-159-10.rspt

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 8, 2002, 15:25:12; Search time 32.48 Seconds
(Without alignments)
87.990 Million cell updates/sec

Title: US-09-865-159-10

Perfect score: 654
Sequence: 1 ALEGTFFSRSQVSRVMAENG.....GGWSCATITVDKFRNGCTD 127

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCrUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	151.5	23.2	154	US-08-486-099-108	Sequence 108, App
2	151.5	23.2	154	US-08-360-107A-118	Sequence 118, App
3	151.5	23.2	154	US-08-484-223B-108	Sequence 108, App
4	151.5	23.2	154	US-08-919-597-108	Sequence 108, App
5	151.5	23.2	154	US-08-475-668A-108	Sequence 108, App
6	151.5	23.2	154	US-08-485-551A-108	Sequence 108, App
7	151.5	23.2	154	US-08-471-913A-108	Sequence 108, App
8	151.5	23.2	154	US-08-485-264A-108	Sequence 108, App
9	96	14.7	17	US-08-084-739-8	Sequence 8, Appli
10	96	14.7	17	US-07-638-492-5	Sequence 5, Appli
11	96	14.7	341	US-08-209-521-11	Sequence 11, Appli
12	90.5	13.8	470	US-09-118-319-8	Sequence 8, Appli
13	81	12.4	14	5445818-6	Patent No. 5445818
14	79	12.1	609	US-08-980-115-11	Sequence 11, Appli
15	75.5	11.5	246	US-08-197-834-7	Sequence 7, Appli
16	73.5	11.2	381	US-09-216-295-22	Sequence 22, Appli
17	73.5	11.2	1996	US-08-804-227C-9	Sequence 9, Appli
18	73.5	11.2	1996	US-08-804-188-3	Sequence 3, Appli
19	71.5	10.9	284	US-08-793-701-39	Sequence 39, Appli
20	71.5	10.9	284	US-08-793-701-41	Sequence 41, Appli
21	71.5	10.9	284	US-08-793-701-57	Sequence 57, Appli
22	71.5	10.9	427	US-08-282-197C-53	Sequence 53, Appli
23	71.5	10.9	562	5258502-2	Patent No. 5258502
24	71	10.9	806	US-08-270-076A-11	Sequence 11, Appli
25	71	10.9	1012	US-08-219-262B-10	Sequence 10, Appli
26	71	10.9	1012	US-09-031-655-10	Sequence 10, Appli
27	70.5	10.8	591	US-09-199-290-7	Sequence 7, Appli

28	70.5	10.8	3012	3	US-08-811-566-2	Sequence 2, Appli
29	70	10.7	312	4	US-09-216-295-21	Sequence 21, Appli
30	70	10.7	352	1	US-07-923-260A-3	Sequence 3, Appli
31	70	10.7	371	4	US-09-104-308-1	Sequence 1, Appli
32	70	10.7	371	4	US-09-321-981-1	Sequence 1, Appli
33	69.5	10.6	409	1	US-08-440-103-21	Sequence 21, Appli
34	69.5	10.6	409	1	US-08-440-103-24	Sequence 24, Appli
35	69.5	10.6	409	1	US-08-440-542-21	Sequence 21, Appli
36	69.5	10.6	409	1	US-08-440-542-24	Sequence 24, Appli
37	69.5	10.6	409	1	US-08-231-368-21	Sequence 21, Appli
38	69.5	10.6	409	1	US-08-231-368-24	Sequence 24, Appli
39	69.5	10.6	409	1	US-08-440-210-21	Sequence 21, Appli
40	69.5	10.6	409	1	US-08-440-210-24	Sequence 24, Appli
41	69.5	10.6	409	4	US-09-046-604-21	Sequence 21, Appli
42	69.5	10.6	409	4	US-09-046-604-24	Sequence 24, Appli
43	69.5	10.6	2396	1	US-08-157-005-2	Sequence 2, Appli
44	69.5	10.6	2396	4	US-08-747-863-2	Sequence 2, Appli
45	69.5	10.6	3144	1	US-08-246-982A-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-08-486-099-108
Sequence 108 Application US/08486099
Patent No. 6013263
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
TITLE OF INVENTION: B VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486, 099
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-031
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 154 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-486-099-108

GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.
 APPLICANT: Barney, Shawn O.
 APPLICANT: Lambert, Dennis M.
 APPLICANT: Peteway, Stephen R.
 APPLICANT: Langlois, Alphonse J.
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
 OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
 TITLE OF INVENTION: TRANSMISSION
 NUMBER OF SEQUENCES: 273
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10036-2711
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentln Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/919,597
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/470,896
 FILING DATE: 06-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Coruzzi, Laura A.
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: 7872-020
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-9741/8864
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 108:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 154 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 US-08-919-597-108

```

STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,668A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 869-9741/9090
TELEFAX: (212) 869-9741/9864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ. ID NO.: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 154 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-475-668A-108

```

[illegible]

```

Query Match          23.2%;   Score 151.5;   DB 3;   Length 154;
Best Local Similarity 31.7%;   Pred. No. 9,4e-09;
Matches    38;   Conservative    25;   Mismatches    44;   Indels    13;   Gaps    3

QY      8 SRSOYSRWMAEAGSLKTAVEACLDGRRNAVGTAA---GCCDGCAGTSSLLTGASOTSOTL 64
       :|::||:::||::||::||::||::||::||::||::||::||::||::||::||::||::
Db      35 ARTQVTRAVSESAKTTAAESAILEGKEIVSATPMDQFDIGFTFESTLLDGSGKSQ--- 91
       ::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::

QY      65 PTNGCVPOVDLPITQTIIATFGGASAISGOLLTWIRDVANGGSC--ATTVDAKFRFN 123
       ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::
Db      92 -----IQVTNDQDTVELVAFLTKRGSSEGAIMGAVITYSRKNDGVNCKIKTPTPMKEN 145
       ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::

RESULT      5
US-08-475-668A-108
; Sequence 108, Application US/08475668A
; Patent No. 6060065
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; TITLE OF INVENTION: Petteway, Stephen R.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
; TRANSMISSION
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP

```

RESULT 6
US-08-485-551A-108
: Sequence 108, Application US/08485551A
: Patent No. 6068973
: GENERAL INFORMATION:
: APPLICANT: Bolognesi, Dani P.
: APPLICANT: Matthews, Thomas J.
: APPLICANT: Wild, Carl T.
: APPLICANT: Barney, Shawn O.
: APPLICANT: Lambert, Dennis M.
: APPLICANT: Peteway, Stephen R.
: APPLICANT: Langlois, Alphonse J.
: TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
: TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
: TITLE OF INVENTION: TRANSMISSION
: NUMBER OF SEQUENCES: 211
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pennie & Edmonds LLP
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: USA
: ZIP: 10036-2711
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,551A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-023
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 154 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-485-551A-108

Query Match 23.2%; Score 151.5; DB 3; Length 154;
Best Local Similarity 31.7%; Pred. No. 9,4e-09;
Matches 38; Conservative 25; Mismatches 44; Indels 13; Gaps 3;

OY 8 SRSQVSRVMAEAGSLKTAFAVACLDGRTAVGTAA---GCCDPCATGSSLLTGASQTSQTL 64
DB 35 ARTQVTRAVSEVSAIKTAFAESALIEGKEIVSATPKPTQYDIGTFESTLIDSGSKSQ--- 91
OY 65 PTNTGVPQVLDPLTQTITATFNGASAAISGQTLTWTVDVNGWSC-ATTVDKFRPN 123
DB 92 -----IQVTDNDQGVLELVATLGKSSGSAIKGAVTVSRKNDGVNCKITPTAMKPN 145

RESULT 7
US-08-471-913A-108
Sequence 108, Application US/08471913A
Patent No. 6093794

GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
NUMBER OF SEQUENCES: 214
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,913A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 154 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-471-913A-108

Query Match 23.2%; Score 151.5; DB 3; Length 154;
Best Local Similarity 31.7%; Pred. No. 9,4e-09;
Matches 38; Conservative 25; Mismatches 44; Indels 13; Gaps 3;

OY 8 SRSQVSRVMAEAGSLKTAFAVACLDGRTAVGTAA---GCCDPCATGSSLLTGASQTSQTL 64
DB 35 ARTQVTRAVSEVSAIKTAFAESALIEGKEIVSATPKPTQYDIGTFESTLIDSGSKSQ--- 91
OY 65 PTNTGVPQVLDPLTQTITATFNGASAAISGQTLTWTVDVNGWSC-ATTVDKFRPN 123
DB 92 -----IQVTDNDQGVLELVATLGKSSGSAIKGAVTVSRKNDGVNCKITPTAMKPN 145

RESULT 8
US-08-485-264A-108
Sequence 108, Application US/08485264A
Patent No. 6228983

GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING
TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 232
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,264A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-021
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 154 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-485-264A-108


```

RESULT 12
US-09-118-319-8
; Sequence 8, Application US/09118319
; Patent No. 6114158
; GENERAL INFORMATION:
; APPLICANT: Li, Xin-Liang
; APPLICANT: Chen, Huizhong
; APPLICANT: Ljungdahl, Lars G.
; TITLE OF INVENTION: Ophiomyces Cellulose
; FILE REFERENCE: 33-98sequence listing
; CURRENT APPLICATION NUMBER: US/09/118,319
; CURRENT FILING DATE: 1998-07-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 470
; TYPE: prt
; ORGANISM: Trichoderma reesei
; US-09-118-319-8

```

RESULT 13
 5445818-6
 : Patent NO. 5445818
 : APPLICANT: HODGES, ROBERT S.; PARANCHYCH, WILLIAM; LEE, KOK K.;
 : PARLMI, SASSTY A.; IRVIN, RANFALL T.; DOIG, PETER C.
 : TITLE OF INVENTION: SYNTHETIC PSEUDOMONAS AERUGINOSA PIILIN
 : PEPTIDE VACCINE AND METHOD OF USE
 : NUMBER OF SEQUENCES: 10
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/07/927,797
 : FILING DATE: 10-AUG-1992
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 344,565
 : FILING DATE: 28-APR-1989
 : SEQ ID NO:6:
 : LENGTH: 14
 5445818-6

```

Query Match          12.4%: Score 81, DB 6, Length 14;
Best Local Similarity 100.0%: Pred. No. 0.012;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      112 CATTVDKFRPNNGC 125
      |||||
      1 CATTVDKFRPNNGC 14

RESULT 14
US-08-980-115-11
; Sequence 11, Application US/08980115
; Patent No. 6266622
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Thomas S.
; APPLICANT: Baxter, John D.
; APPLICANT: Fleeterick, Robert J.
; APPLICANT: Wagner, Richard L.
; APPLICANT: Kushner, Peter J.
; APPLICANT: Apriletti, James W.
; APPLICANT: West, Brian L.
; APPLICANT: Shiau, Andrew K.
; TITLE OF INVENTION: NUCLEAR RECEPTOR LIGANDS AND LIGAND BINDING DOMAINS
; FILE REFERENCE: USAL-246/020US
; CURRENT APPLICATION NUMBER: US/08/980.115
; EARLIER FILING DATE: 1997-11-26
; EARLIER APPLICATION NUMBER: 08/764,870
; EARLIER FILING DATE: 1996-12-13
; EARLIER APPLICATION NUMBER: 60/008,606
; EARLIER FILING DATE: 1995-12-14
; EARLIER APPLICATION NUMBER: 60/008,543
; EARLIER FILING DATE: 1995-12-13
; EARLIER APPLICATION NUMBER: 60/008,540
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 609
; TYPE: PRT
; ORGANISM: Homo sapiens

```

FEATURE:
NAME/KEY: DOMAIN
LOCATION: (295)...(585)
OTHER INFORMATION: minimal ligand binding domain
US-08-980-115-11

Query Match 12.1%; Score 79; DB 4; Length 609;
Best Local Similarity 29.5%; Pred. No. 2.3;
Matches 36; Conservative 11; Mismatches 49; Indels 26; Gaps 5;

QY 1 ALEGEFSRQSVRYMAEAGSLKTAVERACLDGRTAVGTAGCCDPGATGSSLLTGASQT 60
DB 287 SLTTPITTSAMSNVAGLTSQITNAQC-----QVITGLPLVNPAS-----LAGAAAA 335
QY 61 S-----QTLPTNGVPQVLDPLTQTITATFGNGASAAISGOT-----LWTNRDYN 107
DB 336 SALPAQGLQVQVAPQL--LNSQGLIATIGNGPTAIPTASVLPKATVPLFTKTTT 393
QY 108 GG 109
DB 394 QG 395

RESULT 15

US-08-197-834-7
Sequence 7, Application US/08197834
Patent No. 5639455
GENERAL INFORMATION:
APPLICANT: SHIMAMURA, TOSHIRO
APPLICANT: NAKAZAWA, HARUMI
APPLICANT: HAMURO, JUNJI
TITLE OF INVENTION: IMMUNOSUPPRESSANT
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, WAIER & NEUSTADT,
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/197,834
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 028173/1993
FILING DATE: 17-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NO. 5639455man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-661-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 246 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-197-834-7

Query Match 11.5%; Score 75.5; DB 1; Length 246;
Best Local Similarity 27.6%; Pred. No. 1.7;

Matches 29; Conservative 17; Mismatches 52; Indels 7; Gaps 3;
QY 4 GTEFSRQSVRYMAEAGSLKTAVERACLDGRTAVGTAGCCDPGATGSSLLTGASQTSQT 63
DB 69 GTDFTFT-ISTVQAE---DLAVFCCQDDYRSPFTFGSGTKLEIKVDRKSSGSGSEKSTQ 123
QY 64 LPTNGVPQVLDPLTQTITATFGNGASAAISGOTLWTNRDYN 108
DB 124 VKLEESGPILOP--SOTLSLTSFSGFSLTSGMGSWIKOPSG 166

Search completed: February 8, 2002, 15:25:12
Job time: 117 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 8, 2002, 15:32:39 ; Search time 353.09 Seconds
(without alignments)
99.868 Million cell updates/sec

Title: US-09-865-159-10

Perfect score: 654
Sequence: 1 ALEGTFRFSQVSRWMAEGS.....GKMSCTATYDAKFRPNCCTD 127

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3148936 seqs, 277657034 residues

Total number of hits satisfying chosen parameters: 3148936

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending Patents: AA_Main:*

1: /cgn2_6/ptodata/2/paa/PCRUS.COMB.pep:*

2: /cgn2_6/ptodata/2/paa/US07.COMB.pep:*

3: /cgn2_6/ptodata/2/paa/US07.COMB.pep:*

4: /cgn2_6/ptodata/2/paa/US08.COMB.pep:*

5: /cgn2_6/ptodata/2/paa/US08.COMB.pep:*

6: /cgn2_6/ptodata/2/paa/US08.COMB.pep:*

7: /cgn2_6/ptodata/2/paa/US08.COMB.pep:*

8: /cgn2_6/ptodata/2/paa/US08.COMB.pep:*

9: /cgn2_6/ptodata/2/paa/US08.COMB.pep:*

10: /cgn2_6/ptodata/2/paa/US08.COMB.pep:*

11: /cgn2_6/ptodata/2/paa/US08.COMB.pep:*

12: /cgn2_6/ptodata/2/paa/US08.COMB.pep:*

13: /cgn2_6/ptodata/2/paa/US08.COMB.pep:*

14: /cgn2_6/ptodata/2/paa/US09.COMB.pep:*

15: /cgn2_6/ptodata/2/paa/US09.COMB.pep:*

16: /cgn2_6/ptodata/2/paa/US09.COMB.pep:*

17: /cgn2_6/ptodata/2/paa/US09.COMB.pep:*

18: /cgn2_6/ptodata/2/paa/US09.COMB.pep:*

19: /cgn2_6/ptodata/2/paa/US09.COMB.pep:*

20: /cgn2_6/ptodata/2/paa/US09.COMB.pep:*

21: /cgn2_6/ptodata/2/paa/US09.COMB.pep:*

22: /cgn2_6/ptodata/2/paa/US09.COMB.pep:*

23: /cgn2_6/ptodata/2/paa/US09.COMB.pep:*

24: /cgn2_6/ptodata/2/paa/US09.COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	654	100.0	127	US-09-329-884-10	Sequence 10, App1
2	190.5	29.1	153	US-09-540-236-3689	Sequence 3689, App
3	190.5	29.1	153	US-60-128-476-4920	Sequence 4820, App
4	186.5	28.5	127	US-09-329-884-8	Sequence 8, App1
5	151.5	23.2	154	US-08-360-107-118	Sequence 118, App
6	151.5	23.2	154	US-08-470-896-108	Sequence 108, App
7	151.5	23.2	154	US-08-471-913-108	Sequence 108, App
8	151.5	23.2	154	US-08-474-349-108	Sequence 108, App
9	151.5	23.2	154	US-08-474-349A-108	Sequence 108, App

	10	151.5	23.2	154	8	US-08-475-668-108	Sequence 108, App
	11	151.5	23.2	154	8	US-08-484-223-108	Sequence 108, App
	12	151.5	23.2	154	8	US-08-484-223A-108	Sequence 108, App
	13	151.5	23.2	154	8	US-08-485-546-108	Sequence 108, App
	14	151.5	23.2	154	8	US-08-485-546A-108	Sequence 108, App
	15	151.5	23.2	154	8	US-08-485-551-108	Sequence 108, App
	16	151.5	23.2	154	8	US-08-487-266-108	Sequence 108, App
	17	151.5	23.2	154	8	US-08-487-266A-108	Sequence 108, App
	18	151.5	23.2	154	8	US-08-487-355-108	Sequence 108, App
	19	151.5	23.2	154	8	US-08-487-355A-108	Sequence 108, App
	20	151.5	23.2	154	13	US-08-919-600-108	Sequence 108, App
	21	151.5	23.2	154	19	US-09-502-445-108	Sequence 108, App
	22	147	22.5	123	17	US-09-329-884-4	Sequence 4, App1
	23	133.5	20.4	122	17	US-09-329-884-6	Sequence 6, App1
	24	128.5	19.6	169	17	US-09-329-884-14	Sequence 14, App1
	25	127	19.4	169	17	US-09-329-884-12	Sequence 12, App1
	26	123	18.8	129	17	US-09-329-884-2	Sequence 2, App1
	27	121	18.5	84	3	US-07-809-762A-19	Sequence 19, App1
	28	119.5	18.3	139	22	US-09-848-616-140	Sequence 140, App
	29	115	17.6	168	17	US-09-329-884-22	Sequence 22, App1
	30	113.5	17.4	168	17	US-09-329-884-20	Sequence 20, App1
	31	106.5	16.3	82	3	US-07-809-762A-5	Sequence 5, App1
	32	104.5	16.0	175	17	US-09-329-884-18	Sequence 18, App1
	33	103.5	15.8	169	17	US-09-328-352-6277	Sequence 6277, App
	34	103	15.7	175	17	US-09-329-884-16	Sequence 16, App1
	35	97.5	14.9	68	3	US-07-809-762A-17	Sequence 17, App1
	36	97.5	14.9	68	3	US-07-809-762A-4	Sequence 4, App1
	37	95.5	14.6	468	24	US-60-187-409-33	Sequence 33, App1
	38	95.5	14.6	3334	16	US-09-478-081-757	Sequence 757, App
	39	91	13.9	174	16	US-09-252-991A-26702	Sequence 26702, A
	40	90	13.8	605	24	US-60-240-409-616	Sequence 616, App
	41	89.5	13.7	255	18	US-09-417-507-26054	Sequence 26054, A
	42	89	13.6	3880	4	US-08-028-021-1	Sequence 1, App1
	43	88	13.6	11221	21	US-09-778-963-3	Sequence 3, App1
	44	89	13.5	2443	18	US-09-478-081-1011	Sequence 1011, App
	45	87	13.3	2826	1	PCT-US97-17746-50	Sequence 50, App1

ALIGNMENTS

RESULT 1

US-09-329-884-10

Sequence 10, Application US/09329884

GENERAL INFORMATION:

APPLICANT: Irvin, Randall T.

TITLE OF INVENTION: PSEUDOMONAS TREATMENT

FILE REFERENCE: 8900-0008.30

CURRENT FILING DATE: 1999-06-11

EARLIER APPLICATION NUMBER: US 60/089,155

NUMBER OF SEQ ID NOS: 22

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 10

LENGTH: 127

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-329-884-10

Query Match 100.0%; Score 654; DB 17; Length 127;

Best Local Similarity 100.0%; Pred. No. 2e-60;

Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALEGTFRFSQVSRWMAEGSLKTAVEACTLOPGRATVAGTAAGCCPGATGSSLLGASQT 60

DB 1 ALEGTFRFSQVSRWMAEGSLKTAVEACTLOPGRATVAGTAAGCCPGATGSSLLGASQT 60

QY 61 SQTPLNTGVPVLDPLTQTITTFGNGASATISGQTLTWRVNGKMSCTATYDAKF 120

Db 61 SQTLPMTGVPQVLDPLTQTITATFGNGASAAISGQTLTWRDVGWGCATYDAKE 120
 QY 121 RPNCGTD 127
 Db 121 RPNCGTD 127

RESULT 2
 US-09-540-236-3689
 ; Sequence 3689, Application US/09540236
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary L. Breton et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARH
 ; FILE REFERENCE: 2709.2005-001
 ; CURRENT APPLICATION NUMBER: US/09/540,236
 ; CURRENT FILING DATE: 2000-04-04
 ; NUMBER OF SEQ ID NOS: 3840
 ; SEQ ID NO 3689
 ; LENGTH: 153
 ; TYPE: PRN
 ; ORGANISM: M.catarhalls
 US-09-540-236-3689

Query Match 29.1%; Score 190.5; DB 19; Length 153;
 Best Local Similarity 36.8%; Pred. No. 1.3e-11;
 Matches 43; Conservative 15; Mismatches 44; Indels 15; Gaps 3;
 QY 10 SQSVMAEAGSLKTAVEACLODGRATVAGACCCPGATGSSLTGASQTSQTLPTNG 69
 Db 51 AQVNRVMEISQRTAVEMCLGGLN-----AENCKADTINSIDLMG-NKPTVTLPMES- 103
 QY 70 VPQVLDPLTQTITATFGNGASAAISGQTLTWRDVGWGCATYDAKFRPNCCT 126
 Db 104 -----NTESTIKTVFGGNASALHNKQLTWKHSSEKMGKCEIDVDDDFRPGCS 152

RESULT 3
 US-60-128-476-4920
 ; Sequence 4920, Application US/60128476
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary L. Breton et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA
 ; FILE REFERENCE: 107196.139
 ; CURRENT APPLICATION NUMBER: US/60/128,476
 ; CURRENT FILING DATE: 1999-04-09
 ; NUMBER OF SEQ ID NOS: 5002
 ; SEQ ID NO 4920
 ; LENGTH: 153
 ; TYPE: PRN
 ; ORGANISM: Moraxella catarhalls
 US-60-128-476-4920

Query Match 29.1%; Score 190.5; DB 24; Length 153;
 Best Local Similarity 36.8%; Pred. No. 1.3e-11;
 Matches 43; Conservative 15; Mismatches 44; Indels 15; Gaps 3;
 QY 10 SQSVMAEAGSLKTAVEACLODGRATVAGACCCPGATGSSLTGASQTSQTLPTNG 69
 Db 51 AQVNRVMEISQRTAVEMCLGGLN-----AENCKADTINSIDLMG-NKPTVTLPMES- 103
 QY 70 VPQVLDPLTQTITATFGNGASAAISGQTLTWRDVGWGCATYDAKFRPNCCT 126
 Db 104 -----NTESTIKTVFGGNASALHNKQLTWKHSSEKMGKCEIDVDDDFRPGCS 152

RESULT 4
 US-09-329-884-8
 ; Sequence 8, Application US/09329884
 ; GENERAL INFORMATION:

APPLICANT: Irvin, Randall T.
 APPLICANT: Hooges, Robert S.
 TITLE OF INVENTION: PSEUDOMONAS TREATMENT
 TITLE OF INVENTION: COMPOSITION AND METHOD
 FILE REFERENCE: 8900-0008.30
 CURRENT APPLICATION NUMBER: US/09/329,884
 CURRENT FILING DATE: 1999-06-11
 EARLIER APPLICATION NUMBER: US 60/089,155
 NUMBER OF SEQ ID NOS: 22
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 8
 LENGTH: 127
 TYPE: PRN
 ORGANISM: Pseudomonas aeruginosa
 US-09-329-884-8

Query Match 28.5%; Score 186.5; DB 17; Length 127;
 Best Local Similarity 35.4%; Pred. No. 2.8e-11;
 Matches 45; Conservative 25; Mismatches 44; Indels 13; Gaps 3;
 QY 1 ALEGTFSRSQVRYMAEAGSLKTAVEACLODGRATVAGTAA--GCCPGATGSSLTGCA 57
 Db 1 ALEGTFSRSQVRYMAEAGSLKTAVEACLODGRATVAGTAA--GCCPGATGSSLTGCA 60
 QY 58 SQTLPMTGVPQVLDPLTQTITATFGNGASAAISGQTLTWRDVGWGCATYDAK 116
 Db 61 GRSQ-----IQTNKGDTVELVATLKGSSSAIKGAVITVSRNDGVNCKIKRT 111
 QY 117 DAKFRPN 123
 Db 112 PTAKKPN 118

RESULT 5
 US-08-360-107-118
 ; Sequence 118, Application US/08360107
 ; GENERAL INFORMATION:
 ; APPLICANT: Bolognesi, Daniel P.
 ; APPLICANT: Matthews, Thomas J.
 ; APPLICANT: Wild, Carl T.
 ; APPLICANT: Barney, Shawn O.
 ; APPLICANT: Lambert, Dennis M.
 ; APPLICANT: Petteway, Stephen R.
 ; APPLICANT: Langlois, Alphonse J.
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
 ; TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
 ; NUMBER OF SEQUENCES: 137
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Penile & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/360,107
 ; FILING DATE: 20-Dec-1994
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Coruzzi, Laura A.
 ; REGISTRATION NUMBER: 30,742
 ; REFERENCE/DOCKET NUMBER: 7872-013
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 790-9090
 ; TELEFAX: (212) 869-9741/8864


```

? APPLICANT: Petteway, Stephen R.
? APPLICANT: Langlois, Alphonse J.
? TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
? TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA
? TITLE OF INVENTION: VIRUS TRANSMISSION
? NUMBER OF SEQUENCES: 517
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Pennie & Edmonds
? STREET: 1155 Avenue of the Americas
? CITY: New York
? STATE: New York
? COUNTRY: USA
? ZIP: 10036-2711
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/474,349A
? FILING DATE: 07-JUN-1995
? CLASSIFICATION:
? ATTORNEY/AGENT INFORMATION:
? NAME: Cornuzzi, Laura A.
? REGISTRATION NUMBER: 30,742
? REFERENCE/DOCKET NUMBER: 7872-024
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (212) 790-9090
? TELEFAX: (212) 869-9741/8864
? TELEX: 66141 PENNTE
? INFORMATION FOR SEQ ID NO: 108:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 154 amino acids
? TYPE: amino acid
? STRANDEDNESS:
? TOPOLOGY: unknown
? MOLECULE TYPE: protein
? US-08-474-349A-108

Query Match      23.2%, Score 151.5; DB 8; Length 154;
Best Local Similarity 31.7%; Pred. No. 1.7e-07;
Matches 38; Conservative 25; Mismatches 44; Indels 13; Gaps 3;

QY      8 SRSQYSRMAERAGSLKTVEACLDGRTAVGTAA---GCCDPGATGSLLTGASQTSOTL 64
Db      35 AKTVQTRAVSESAIKTAESAILEGKIVSSAPPKDYDIGFTESILLDGGSKSQ--- 91
        ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      65 PTNTGVPAVLPLTQTTLIAFPNGASAALISGQLTFWTRDVNGWGWC-ATTVAKKRPN 123
Db      92 -----IQVDNDQCGVETVALTKRSSGAIKGAVITVRNRNDGWNCIKITPTLAWKP 145
        || | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 10
? Sequence 108, Application US/08475668
? GENERAL INFORMATION:
? APPLICANT: Bolognesi, Dani P.
? APPLICANT: Matthews, Thomas J.
? APPLICANT: Wild, Carl T.
? APPLICANT: Barney, Shawn O.
? APPLICANT: Lambert, Dennis M.
? APPLICANT: Petteway, Stephen R.
? APPLICANT: Langlois, Alphonse J.
? TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
? TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA
? NUMBER OF SEQUENCES: 209
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Pennie & Edmonds
? STREET: 1155 Avenue of the Americas
? CITY: New York
? STATE: New York

```


S-08-485-551-108

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 8, 2002, 15:26:39 ; Search time 37.1 Seconds
(without alignments)
152.410 Million cell updates/sec

Title: US-09-865-159-10

Perfect score: 654
Sequence: 1 ALEGTFRSRSOVSRYMAEAGS.....GWSGATTVDAKFRNGCTD 127

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 211743 seqs, 44522877 residues

Total number of hits satisfying chosen parameters: 211743

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

Pending Patents AA New:
1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep.*
2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep.*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep.*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep.*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	654	100.0	127	5	US-09-865-159-10 Sequence 10, Appl
2	186.5	28.5	127	5	US-09-865-159-8 Sequence 8, Appl
3	147	22.5	123	5	US-09-865-159-4 Sequence 4, Appl
4	133.5	20.4	122	5	US-09-865-159-6 Sequence 6, Appl
5	128.5	19.6	169	5	US-09-865-159-14 Sequence 14, Appl
6	127	19.4	129	5	US-09-865-159-12 Sequence 12, Appl
7	123	18.8	129	5	US-09-865-159-2 Sequence 2, Appl
8	115	17.6	168	5	US-09-865-159-22 Sequence 22, Appl
9	113.5	17.4	168	5	US-09-865-159-20 Sequence 20, Appl
10	104.5	16.0	175	5	US-09-865-159-18 Sequence 18, Appl
11	103	15.7	175	5	US-09-865-159-16 Sequence 16, Appl
12	90.5	13.8	1076	6	US-10-028-072-219 Sequence 219, Appl
13	90	13.5	605	5	US-09-976-594-616 Sequence 616, Appl
14	81.5	12.3	377	5	US-09-500-746-20 Sequence 20, Appl
15	80.5	12.3	585	5	US-09-817-774-24 Sequence 24, Appl
16	78	11.9	209	5	US-09-605-703B-2320 Sequence 2320, Appl
17	77.5	11.9	204	6	US-10-005-368-139 Sequence 139, Appl
18	77	11.7	525	5	US-09-605-703B-2606 Sequence 2606, Appl
19	76.5	11.7	303	4	US-08-737-904H-58 Sequence 58, Appl
20	76	11.6	1497	5	US-09-890-677-3 Sequence 3, Appl
21	75.5	11.5	222	5	US-09-675-784A-13920 Sequence 13920, Appl
22	75	11.5	249	5	US-09-707-921-6 Sequence 6, Appl
23	75	11.5	288	5	US-09-707-921-9 Sequence 9, Appl
24	75	11.5	300	5	US-09-707-921-12 Sequence 12, Appl
25	75	11.5	975	5	US-09-886-055-431 Sequence 431, Appl
26	74.5	11.4	202	5	US-09-594-595B-251 Sequence 251, Appl

27	74.5	11.4	304	7	US-60-336-968-9 Sequence 9, Appl
28	74.5	11.4	2344	5	US-09-815-242-12713 Sequence 12713, A
29	74	11.3	684	5	US-09-303-518D-721 Sequence 721, Appl
30	74	11.3	1302	5	US-09-935-384-764 Sequence 764, Appl
31	73.5	11.2	365	5	US-09-708-427-3688 Sequence 3688, Appl
32	73.5	11.2	402	5	US-09-708-427-3687 Sequence 3687, Appl
33	73	11.2	463	6	US-10-006-867-86 Sequence 86, Appl
34	73	11.2	4315	1	PCT-US01-27760-811 Sequence 811, Appl
35	73	11.2	4315	1	PCT-US01-27760A-811 Sequence 811, Appl
36	72.5	11.1	160	5	US-09-637-780B-152 Sequence 152, Appl
37	72.5	11.1	496	5	US-09-708-427-50797 Sequence 50797, A
38	72	11.0	425	5	US-09-500-746-18 Sequence 18, Appl
39	71.5	10.9	350	5	US-09-605-703B-916 Sequence 916, Appl
40	71.5	10.9	562	5	US-09-801-368-82 Sequence 82, Appl
41	71.5	10.9	562	5	US-09-487-358-87 Sequence 82, Appl
42	71.5	10.9	914	5	US-09-975-143-47 Sequence 47, Appl
43	71	10.9	791	6	US-10-015-127-10930 Sequence 10930, A
44	70.5	10.8	131	5	US-09-708-427-83496 Sequence 83496, A
45	70.5	10.8	200	5	US-09-999-201-2 Sequence 2, Appl

ALIGNMENTS

```
RESULT 1
US-09-865-159-10
: Sequence 10, Application US/09865159
: GENERAL INFORMATION:
: APPLICANT: Irvin, Randall T.
: TITLE OF INVENTION: PSEUDOMONAS TREATMENT
: FILE REFERENCE: 8900-0008.30
: CURRENT APPLICATION NUMBER: US/09/865,159
: PRIOR FILING DATE: 2001-05-24
: PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329,884
: NUMBER OF SEQ ID NOS: 22
: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ ID NO 10
: LENGTH: 127
: TYPE: PRT
: ORGANISM: Pseudomonas aeruginosa
US-09-865-159-10

Query Match      100.0%; Score 654; DB 5; Length 127;
Best Local Similarity 100.0%; Pred. No. 3.4e-57;
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALEGTFRSRSOVSRYMAEAGSLKTAVEACLDGRRAVGTAGACDPCATGSSLTGASQT 60
    |||||||
Db 1 ALEGTFRSRSOVSRYMAEAGSLKTAVEACLDGRRAVGTAGACDPCATGSSLTGASQT 60

QY 61 SQTLPNMGVQVLDPLTQTTITPCNGASAAISGTLTWRVNGSGWGCATTVDKFF 120
    |||||||
Db 61 SQTLPNMGVQVLDPLTQTTITPCNGASAAISGTLTWRVNGSGWGCATTVDKFF 120

QY 121 RPNGCTD 127
    |||||||
Db 121 RPNGCTD 127

RESULT 2
US-09-865-159-8
: Sequence 8, Application US/09865159
: GENERAL INFORMATION:
: APPLICANT: Irvin, Randall T.
: TITLE OF INVENTION: PSEUDOMONAS TREATMENT
: FILE REFERENCE: 8900-0008.30
: CURRENT APPLICATION NUMBER: US/09/865,159
```

Page 2

RESULT 4
US-09-865-159-6
; Sequence 6, Application US/09865159
; GENERAL INFORMATION:
; APPLICANT: Irvin, Randall T.

```

? Sequence 14, Application US/09865159
? GENERAL INFORMATION:
?
? APPLICANT: Irvin, Randall T.
?
? TITLE OF INVENTION: PSEUDOMONAS TREATMENT
?
? FILE REFERENCE: 8900-0008.30
?
? CURRENT APPLICATION NUMBER: US/09/865.159
?
? PRIOR FILING DATE: 2001-05-24
?
? PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329,888
?
? NUMBER OF SEQ ID NOS: 22
?
? SOFTWARE: FASTSEQ for Windows Version 3.0
?
? SEQ ID NO 14
?
? LENGTH: 169
?
? TYPE: PR1
?
? ORGANISM: Pseudomonas aeruginosa
?
? US-09-865-159-14

```

QY	114	TTVDAKFRPNGCT	126
	:	: :	
Db	156	SDQDEQFI PKGS	168

RESULT 6
US-09-865-159-12
; Sequence 12, Application US/09865159
; GENERAL INFORMATION:
; APPLICANT: Irvin, Randall T.
; TITLE OF INVENTION: PSEUDOMONAS TREATMENT
; FILE REFERENCE: 8900-0008.30
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329,884
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 169
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-865-159-12

Query Match 19.4%; Score 127; DB 5; Length 169;
Best Local Similarity 31.5%; Pred. No. 2,3e-05;
Matches 40; Conservative 16; Mismatches 59; Indels 12; Gaps 5;

QY 4 GTEFSRQSVRYMAEAGSLKTAVEACLDG---RTAVGTAGQCDPGATGSSLLTGASQT 60
DB 50 GGEFARSEGASALASVNPDKTVEEALSRGMSVKSQGTGT-----EDATKKEVPLGVAD 103
QY 61 SQTLPNTNGVQVLDPLTQTITITFNGGASAAISGQTLTWTRD-VNGGSCATVPAK 119
DB 104 ANKGTITALKRDPADG-TADITLFTTGG-GAGPKNKGIITLITRAADGLMKCTSDODEQ 161
QY 120 FRPNCGT 126
DB 162 FIPKCS 168

RESULT 7
US-09-865-159-2
; Sequence 2, Application US/09865159
; GENERAL INFORMATION:
; APPLICANT: Irvin, Randall T.
; TITLE OF INVENTION: PSEUDOMONAS TREATMENT
; FILE REFERENCE: 8900-0008.30
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329,884
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-865-159-2

Query Match 18.8%; Score 123; DB 5; Length 129;
Best Local Similarity 30.7%; Pred. No. 4,2e-05;
Matches 42; Conservative 20; Mismatches 47; Indels 28; Gaps 7;

QY 1 ALEGTFSRQSVRYMAEAGSLKTAV-EACLDGRTAVGTAG---OCDPGATG---SSL 53
DB 1 ALEGTFSRQSVRYMAEAGSLKTAV-EACLDGRTAVGTAG---OCDPGATG---SSL 53
QY 54 LTGASQTSQTLPTNTNGVQVLDPLTQTITITF-GNGASAAISGQTLTWTRD-VN 109
DB 61 TTGCTAA-----SGGCTIVATMKASDVATPLRGKTLTLLTGNADKGSY 104

QY 110 -WSCATVDKFRPNCG 125
DB 105 TWACTSNADNKKYLPKTC 121

RESULT 8
US-09-865-159-22
; Sequence 22, Application US/09865159
; GENERAL INFORMATION:
; APPLICANT: Irvin, Randall T.
; TITLE OF INVENTION: PSEUDOMONAS TREATMENT
; FILE REFERENCE: 8900-0008.30
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329,884
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-865-159-22

Query Match 17.6%; Score 115; DB 5; Length 168;
Best Local Similarity 30.3%; Pred. No. 0.00035;
Matches 40; Conservative 17; Mismatches 57; Indels 18; Gaps 5;

QY 1 ALE---GTEFSRQSVRYMAEAGSLKTAVEACLDG---RTAVGTAGQCDPGATGSS 53
DB 44 ALEKGGGGEFARSEGASALATINPLKTVESLSRIGSKIKIGTTA-----STATET 97
QY 54 LTGASQTSQTLPTNTNGVQVLDPLTQTITITFNGGASAAISG-QTLTWTRDVGWGC 112
DB 98 YAGVEPDANKL-----GVLAVIDESGAGDITFTFOTGTSSPKNAKVIITLNTADGVWAC 153
QY 113 ATTVDKFRPNCG 124
DB 154 KSTQDPMFTPKG 165

RESULT 9
US-09-865-159-20
; Sequence 20, Application US/09865159
; GENERAL INFORMATION:
; APPLICANT: Irvin, Randall T.
; TITLE OF INVENTION: PSEUDOMONAS TREATMENT
; FILE REFERENCE: 8900-0008.30
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329,884
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-865-159-20

Query Match 17.4%; Score 113.5; DB 5; Length 168;
Best Local Similarity 29.4%; Pred. No. 0.00049;
Matches 37; Conservative 17; Mismatches 57; Indels 15; Gaps 4;

QY 4 GTEFSRQSVRYMAEAGSLKTAVEACLDG---RTAVGTAGQCDPGATGSSLLTGASQ 59
DB 50 GGEFARSEGASALATINPLKTVESLSRIGSKIKIGTTA-----STATETVAGVPE 103

QY 60 TSQTLPTNGVPOVLDPLTTOTLTATFGNGSAISG-QTLTWRDVGNGSCATTYDA 118
 Db 104 DANKL-----GVIAVAIEDSGADITFTQTGTSSPKNAKVTTLNRTADGVWACKSTODP 159
 QY 119 KFRPNG 124
 Db 160 METPKG 165

RESULT 10

US-09-865-159-16
 ; Sequence 18, Application US/09865159
 ; GENERAL INFORMATION:
 ; APPLICANT: Irvin, Randall T.
 ; APPLICANT: Hodges, Robert S.
 ; TITLE OF INVENTION: PSEUDOMONAS TREATMENT
 ; FILE REFERENCE: 8900-0008.30
 ; CURRENT APPLICATION NUMBER: US/09/865,159
 ; CURRENT FILING DATE: 2001-05-24
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329,884
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 18
 ; LENGTH: 175
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-865-159-18

Query Match

Best Local Similarity 16.0%; Score 104.5; DB 5; Length 175;
 Matches 41; Conservative 20; Mismatches 48; Indels 31; Gaps 8;

QY 1 ALE---GTEFSRSQVSWMAEAGSLKTAV-EACLDGRTAVGTAG---QCDPGATG--- 50
 Db 44 ALKKGGGGERRARQSLERMTLASGLTKVSDIFSGDSCPANTAAAGIEKPTDINGKYV 103
 QY 51 SSLTIGASOTSQTLPTNGVPOVLDPLTTOTLTATF-GNGASAAISGQTLTWT-RDVG 108
 Db 104 AKYTTGGTAA-----SSGCTIVATMKASDVATPLRGKTLTLTGNADK 147
 QY 109 G---WSCATTYAKFRPNC 125
 Db 148 GSTWACTSNADKYLPTKC 167

RESULT 11

US-09-865-159-16
 ; Sequence 16, Application US/09865159
 ; GENERAL INFORMATION:
 ; APPLICANT: Irvin, Randall T.
 ; APPLICANT: Hodges, Robert S.
 ; TITLE OF INVENTION: PSEUDOMONAS TREATMENT
 ; FILE REFERENCE: 8900-0008.30
 ; CURRENT APPLICATION NUMBER: US/09/865,159
 ; CURRENT FILING DATE: 2001-05-24
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329,884
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 16
 ; LENGTH: 175
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-865-159-16

Query Match 15.7%; Score 103; DB 5; Length 175;
 Best Local Similarity 28.4%; Pred. No. 0.0055;

Matches 38; Conservative 20; Mismatches 48; Indels 28; Gaps 7;

QY 4 GTEFSRSQVSWMAEAGSLKTAV-EACLDGRTAVGTAG---QCDPGATG---SSLTNG 56
 Db 50 GGEFARQSLERMTLASGLTKVSDIFSGDSCPANTAAAGIEKPTDINGRYVAKVTG 109
 QY 57 ASQTSQTLPTNGVPOVLDPLTTOTLTATF-GNGASAAISGQTLTWT-RDVGNG---WS 111
 Db 110 GTAA-----SSGCTIVATMKASDVATPLRGKTLTLTGNADKSYTWA 153
 QY 112 CATTYAKFRPNC 125
 Db 154 CTSNADNKYLPTKC 167

RESULT 12

US-10-028-072-219
 ; Sequence 219, Application US/10028072
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Beresini, Maureen
 ; APPLICANT: DeForge, Laura
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Geo, Wei-Qiang
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Sherwood, Steven
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K
 ; APPLICANT: Wood, William
 ; APPLICANT: Zhang
 ; TITLE OF INVENTION:
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: US/10/028,072
 ; PRIOR APPLICATION NUMBER: 60/049911
 ; PRIOR FILING DATE: 1997-06-18
 ; PRIOR APPLICATION NUMBER: 60/056974
 ; PRIOR FILING DATE: 1997-08-26
 ; PRIOR APPLICATION NUMBER: 60/059113
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/059115
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/059117
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/059122
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/059184
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/059263
 ; PRIOR FILING DATE: 1997-09-18
 ; PRIOR APPLICATION NUMBER: 60/059352
 ; PRIOR FILING DATE: 1997-09-19
 ; PRIOR APPLICATION NUMBER: 60/059588
 ; PRIOR FILING DATE: 1997-09-19
 ; PRIOR APPLICATION NUMBER: 60/059836
 ; PRIOR FILING DATE: 1997-09-24
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/062285
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/062287
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/062814
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR APPLICATION NUMBER: 60/062816
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR APPLICATION NUMBER: 60/063045

PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063082
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/063127
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063327
PRIOR FILING DATE: 1997-10-27
PRIOR APPLICATION NUMBER: 60/063329
PRIOR FILING DATE: 1997-10-27
PRIOR APPLICATION NUMBER: 60/063550
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063561
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063704
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063733
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063735
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063738
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063755
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064248
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/064809
PRIOR FILING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065846
PRIOR FILING DATE: 1997-11-17
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/066453
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/066511
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/069212
PRIOR FILING DATE: 1997-12-11
PRIOR APPLICATION NUMBER: 60/069278
PRIOR FILING DATE: 1997-12-11
PRIOR APPLICATION NUMBER: 60/069334
PRIOR FILING DATE: 1997-12-11
PRIOR APPLICATION NUMBER: 60/069694
PRIOR FILING DATE: 1997-12-16
PRIOR APPLICATION NUMBER: 60/072320
PRIOR FILING DATE: 1998-01-23
PRIOR APPLICATION NUMBER: 60/073612
PRIOR FILING DATE: 1998-02-04
PRIOR APPLICATION NUMBER: 60/074086
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/074092
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-02-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081695
PRIOR FILING DATE: 1998-04-14

PRIOR APPLICATION NUMBER: 60/081817
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081818
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082999
PRIOR FILING DATE: 1998-04-24
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083545
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084627
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084637
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/085149
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085338
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085339
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/086414
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/086430
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088730
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088741
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 19/98-06-11
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090538
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/093339

Query Match

13.8%; Score 90.5; DB 6; Length 1076;

Best Local Similarity 29.7%; Pred. No. 0.76;
Matches 33; Conservative 7; Mismatches 54; Indels 17; Gaps 4;

OY 17 AEASLKTAVEACLDGRTAVGTAGAGCCDPGATGSSLLTGASQ---TSQTLPTNTGVPO 72

Db 908 AATTAATGTTACTGACACTTAATATAGATGTTATGATGATGCTGTTAGCTTT 967

OY 73 VLDELTTQTTTIAF-----FENGASAAISGQTLTWTBVDVNGWSCATT 115

Db 968 GAAATTTGTAATATATGATGCCAGGTGTGAATGACTGACT---TAACACATT 1013

RESULT 13

US-09-976-594-616

; Sequence 616, Application US/09976594

; GENERAL INFORMATION:

; APPLICANT: Furness, Michael

; APPLICANT: Buchbinder, Jenny

; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS

; FILE REFERENCE: PA-0041 US

; CURRENT APPLICATION NUMBER: US/09/976,594

; CURRENT FILING DATE: 2001-10-12

; PRIOR APPLICATION NUMBER: 60/240,409

; PRIOR FILING DATE: 2000-10-12

; NUMBER OF SEQ ID NOS: 1143

; SOFTWARE: PERL Program

; SEQ ID NO 616

; LENGTH: 605

; TYPE: PRT

; ORGANISM: Homo sapiens

; NAME/KEY: misc_feature

; OTHER INFORMATION: Incyte ID No.: 1692213CB1

; NAME/KEY: unsure

; LOCATION: 596

; OTHER INFORMATION: unknown or other

US-09-976-594-616

Query Match 13.8%; Score 90; DB 5; Length 605;
Best Local Similarity 30.0%; Pred. No. 0.44;

Matches 33; Conservative 6; Mismatches 41; Indels 30; Gaps 4;

OY 17 AEGSLKTAVEACLDGRTAVGTAGAGCCDPGATGSSLLTGASQTSQTLPTNTGVPOVDLP 76

Db 419 AGAAATTAATATC---ATATGAAGAC-----TGAAATAGTTTATACATTTTG 464

OY 77 LTTQTTIATFNGASAAISGQTLTWTBVDVNGWSCATTVDKFRPNCGT 126

Db 465 TTCTCTTAAGATATACATAT-----TCTTTGA-----GCT 498

RESULT 14

US-09-500-746-20

; Sequence 20, Application US/09500746

; GENERAL INFORMATION:

; APPLICANT: Winchester, Robert J.

; APPLICANT: Guiko, Percio

; APPLICANT: Seki, Tetsunori

; TITLE OF INVENTION: USES OF INHIBITORS FOR THE ACTIVATION OF CXCR4 RECEPTOR BY SDF-1

; FILE REFERENCE: 0575/57005-B

; CURRENT APPLICATION NUMBER: US/09/500,746

; CURRENT FILING DATE: 2000-02-09

; NUMBER OF SEQ ID NOS: 23

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 20

; LENGTH: 377

; TYPE: PRT

; ORGANISM: Human

US-09-500-746-20

Query Match 12.5%; Score 81.5; DB 5; Length 377;
Best Local Similarity 32.1%; Pred. No. 1.7;

Matches 36; Conservative 6; Mismatches 53; Indels 17; Gaps 4;

OY 19 AGSLKTAVEACLDGRTAVGTAGAGCCDPGATGSSLLTGASQTSQTLPTNTGVPOVDLP 78

Db 231 AAACCTAAAC-----CTGTGAG---AGATGAAGGCANTGTTTGTGTGAGAGGGGCC 282

OY 79 TQTTIATFNGASAAISGQTLTWT---RDVNGWSCATTVDKFRPNCGT 126

Db 283 TTAAACCATGAGACAGGTGTGTGTGTGGGTGGCAGCATGNGAT-----CT 329

RESULT 15

US-09-817-774-24

; Sequence 24, Application US/09817774

; GENERAL INFORMATION:

; APPLICANT: CHOE, Sunghwa

; APPLICANT: FELDMANN A., Kenneth

; TITLE OF INVENTION: Dwt5 MUTANTS

; FILE REFERENCE: 2225-0020 / 91020.002

; CURRENT APPLICATION NUMBER: US/09/817,774

; CURRENT FILING DATE: 2001-03-26

; PRIOR APPLICATION NUMBER: 60/192,202

; PRIOR FILING DATE: 2000-03-27

; NUMBER OF SEQ ID NOS: 45

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 24

; LENGTH: 585

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: LBR-CHICKEN

US-09-817-774-24

Query Match 12.3%; Score 80.5; DB 5; Length 585;
Best Local Similarity 35.0%; Pred. No. 3.6;

Matches 35; Conservative 4; Mismatches 32; Indels 29; Gaps 6;

OY 19 AGSLKTAVEACLDGRTAVGTAGAGCCDPGAT-GSSLLTGASQTSQTLPTNTGVPOVDLP 77

Db 349 AGAATTA--AC---GCATTACAGCCATGATGATGACGCGCTCTCTAGTGGG----- 395

OY 78 TQTTIATFNGASAAISGQTLTWTBVDVNGWS--CAT 115

Db 396 -----GGAGACAGTATGTTT---GGGTTCCATT 422

Search completed: February 8, 2002, 15:26:39
Job time: 204 sec

Fri Feb 8 15:44:48 2002

us-09-865-159-10.rapn

Page 7

